


```

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 2127-104
; CURRENT APPLICATION NUMBER: PCT/US01/14827
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/577,408
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 16102
; SEQ ID NO 14753
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(108)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
PCT-US01-14827-14753

Query Match 100.0%; Score 29; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 3.3e+02; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 2127-104
; CURRENT APPLICATION NUMBER: PCT/US01/14827
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/577,408
; PRIOR FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 16102
; SOFTWARE: Custom
; SEQ ID NO 12024
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (30)..(41)
; OTHER INFORMATION: PROTEIN SPORULATION REPEAT PRECU domain identified by
; OTHER INFORMATION: eMATRIX, accession number PD02283B, p-value=7.857e-09, raw score
; OTHER INFORMATION: 8.67
PCT-US01-14827-12024

Query Match 100.0%; Score 29; DB 1; Length 75;
Best Local Similarity 100.0%; Pred. No. 2.2e+02; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; GENERAL INFORMATION:
; APPLICANT: Bonazzi, Vivien
; TITLE OF INVENTION: ISOLATED KINASE PROTEINS, NUCLEIC ACID
; FILE REFERENCE: CL00064
; CURRENT APPLICATION NUMBER: US/60/146,315
; CURRENT FILING DATE: 1999-07-29
; NUMBER OF SEQ ID NOS: 1086
; SEQ ID NO 856
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Drosophila
; SEQ ID NO 60-146-315-866

Query Match 100.0%; Score 29; DB 26; Length 67;
Best Local Similarity 100.0%; Pred. No. 1.9e+02; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 2127-104
; CURRENT APPLICATION NUMBER: PCT/US01/14827
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/577,408
; PRIOR FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 16102
; SEQ ID NO 16 LEPRAS 21
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(108)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
PCT-US01-14827-14753

Query Match 100.0%; Score 29; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 3.3e+02; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 2127-066
; CURRENT APPLICATION NUMBER: PCT/US01/08656
; CURRENT FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: 09/522, 929
; PRIOR FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: Custom
; SEQ ID NO 7642
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
; SEQ ID NO 35 LEPRAS 40
PCT-US01-08656-7642

Query Match 100.0%; Score 29; DB 1; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.6e+02; Pred. No. 3.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PH01
; CURRENT APPLICATION NUMBER: US/09/758,472
; CURRENT FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/179, 065
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 628
; SEQ ID NO 1 LEPRAS 6
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(119)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
PCT-US01-14827-14753

Query Match 100.0%; Score 29; DB 1; Length 75;
Best Local Similarity 100.0%; Pred. No. 2.2e+02; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PH01
; CURRENT APPLICATION NUMBER: US/09/758,472
; CURRENT FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/179, 065
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 628
; SEQ ID NO 1 LEPRAS 6
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(75)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
PCT-US01-14827-14753

```

PRIOR FILING DATE: 2000-02-04
 NUMBER OF SEQ ID NOS: 9632
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 5581
 LENGTH: 153

ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: SITE
 LOCATION: (115)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 NAME/KEY: SITE
 LOCATION: (122)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 NAME/KEY: SITE
 LOCATION: (123)

Query Match 100.0%; Score 29; DB 21; Length 153;
 Best Local Similarity 100.0%; Pred. No. 4.8e+02; Matches 6; Conservative 0; Mismatches 0;
 Matches 6; Conservative 0; Mismatches 0;
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 US-09-758-472-5581

Query Match 100.0%; Score 29; DB 12; Length 256;
 Best Local Similarity 100.0%; Pred. No. 8.5e+02; Matches 6; Conservative 0; Mismatches 0;
 Matches 6; Conservative 0; Mismatches 0;

Qy 1 LEPRAS 6
 Db 146 LEPRAS 151

RESULT 7
 US-08-878-322-11
 Sequence 11, Application US/08878322

GENERAL INFORMATION:
 APPLICANT: Sheppard, Paul O.
 APPLICANT: Jelinek, Laura J.
 APPLICANT: Whitmore, Theodore E.

APPLICANT: Blumberg, Hal
 TITLE OF INVENTION: MAMMALIAN ZNEU1
 NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:
 ADDRESSEE: ZymoGenetics, Inc.
 STREET: 1201 Eastlake Ave. East

CITY: Seattle
 STATE: WA
 COUNTRY: USA

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS

COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/099,295
 FILING DATE: 2000-03-22
 CLASSIFICATION:
 PRIOR APPLICATION DATA:

APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:

NAME: Lunn, Paul G
 REGISTRATION NUMBER: 32,743
 REFERENCE/DOCKET NUMBER: 97-28

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 206-442-6627
 TELEFAX: 206-442-6678

INFORMATION FOR SEQ ID NO: 11:
 INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:
 LENGTH: 256 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear

MOLECULE TYPE: protein
 US-09-099-295-11

REFERENCE/DOCKET NUMBER: 32,743
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 206-442-6627
 TELEFAX: 206-442-6678

INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 256 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear

ORIGINAL SOURCE:
 US-08-878-322-11
 RESULT 8
 US-09-099-295-11
 Sequence 11, Application US/09099295
 GENERAL INFORMATION:
 APPLICANT: Sheppard, Paul O.
 APPLICANT: Jelinek, Laura J.
 APPLICANT: Whitmore, Theodore E.
 APPLICANT: Blumberg, Hal
 APPLICANT: Leiner, Joyce M.
 TITLE OF INVENTION: MAMMALIAN NEURO-GROWTH FACTOR LIKE
 NUMBER OF SEQUENCES: 24
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: ZymoGenetics
 STREET: 1201 Eastlake Ave East
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98102
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/099,295
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:

NAME: Lunn, Paul G
 REGISTRATION NUMBER: 32,743
 REFERENCE/DOCKET NUMBER: 97-28

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 206-442-6627
 TELEFAX: 206-442-6678

INFORMATION FOR SEQ ID NO: 11:
 INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:
 LENGTH: 256 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear

MOLECULE TYPE: protein
 US-09-099-295-11

REFERENCE/DOCKET NUMBER: 32,743
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 206-442-6627
 TELEFAX: 206-442-6678

INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 256 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear

ORIGINAL SOURCE:
 US-09-099-295-11
 RESULT 9
 US-09-099-295-11

```

; Sequence 11, Application US/09852472
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Jelinek, Laura J.
; TITLE OF INVENTION: Mammalian Neuro-Growth Factor Like
; TITLE OF INVENTION: Protein
; FILE REFERENCE: 97-28C1
; CURRENT APPLICATION NUMBER: US/09/852,472
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 09/099,295
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/050,143
; PRIOR FILING DATE: 1997-06-18
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-852-472-11

Query Match          100.0%;  Score 29;  DB 22;  Length 256;
Best Local Similarity 100.0%;  Pred. No. 8.5e+02;  Indels 0;  Gaps 0;
Matches 6;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy      1 LEPRAS 6
Db      146 LEPRAS 151

RESULT 10
US-09-758-440-688
; Sequence 688, Application US/09758440
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic acids, Proteins, and Antibodies
; FILE REFERENCE: PM015
; CURRENT APPLICATION NUMBER: US/09/758,440
; CURRENT FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 832
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 688
; LENGTH: 258
; TYPE: PRT
; FEATURE:
; ORGANISM: Homo sapiens
; NAME/KEY: SITE
; LOCATION: (8)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; US-09-758-440-688

Query Match          100.0%;  Score 29;  DB 21;  Length 258;
Best Local Similarity 100.0%;  Pred. No. 8.6e+02;  Indels 0;  Gaps 0;
Matches 6;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy      1 LEPRAS 6
Db      146 LEPRAS 151

RESULT 11
US-09-902-540-13318
; Sequence 13318, Application US/09902540
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.

Query Match          100.0%;  Score 29;  DB 23;  Length 421;
Best Local Similarity 100.0%;  Pred. No. 1.5e+03;  Indels 0;  Gaps 0;
Matches 6;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy      1 LEPRAS 6
Db      406 LEPRAS 411

RESULT 12
US-09-270-767-57034
; Sequence 57034, Application US/09270767
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7320-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 57034
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
; US-09-270-767-57034

Query Match          100.0%;  Score 29;  DB 16;  Length 439;
Best Local Similarity 100.0%;  Pred. No. 1.6e+03;  Indels 0;  Gaps 0;
Matches 6;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy      1 LEPRAS 6
Db      196 LEPRAS 201

RESULT 13
US-09-270-849B-180914
; Sequence 180914, Application US/09270849B
; GENERAL INFORMATION:
; APPLICANT: Swimmer et al.
; TITLE OF INVENTION: Insect genome survey devices
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/270,849B
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 19540
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 180914
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: at any location having Xaa, Xaa means any amino acid
; OTHER INFORMATION: at any location having Xaa, Xaa means any amino acid
; US-09-270-849B-180914

```

Query Match 100.0%; Score 29; DB 16; Length 439;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03; Length 439;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEPRAS 6
 Db 196 LEPRAS 201

RESULT 14
 US-60-206-047-406
 Sequence 406, Application US/60206047
 GENERAL INFORMATION:
 APPLICANT: Beasley, Ellen
 TITLE OF INVENTION: ISOLATED HUMAN PHASE I DRUG-METABOLIZING
 PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
 DRUG-METABOLIZING PHASE I PROTEINS, AND USES THEREOF
 FILE REFERENCE: CL000570
 CURRENT APPLICATION NUMBER: US/60/206, 047
 CURRENT FILING DATE: 2000-05-22
 NUMBER OF SEQ ID NOS: 456
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 406
 LENGTH: 471
 TYPE: PRT
 ORGANISM: HUMAN
 US-60-206-047-406

Query Match 100.0%; Score 29; DB 26; Length 471;
 Best Local Similarity 100.0%; Pred. No. 1.7e+03; Length 471;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEPRAS 6
 Db 282 LEPRAS 287

RESULT 15
 US-60-171-625-531
 Sequence 531, Application US/60171625
 GENERAL INFORMATION:
 APPLICANT: Skupski, Marian
 TITLE OF INVENTION: ISOLATED DROSOPHILA PROTEINS THAT SHOW
 HIGH HOMOLOGY TO KNOWN HUMAN DISEASE PROTEINS, AND USES
 OF INVENTION: THEREOF
 FILE REFERENCE: CL000179
 CURRENT APPLICATION NUMBER: US/60/171,625
 CURRENT FILING DATE: 1999-12-23
 NUMBER OF SEQ ID NOS: 579
 SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ ID NO 531
 LENGTH: 634
 TYPE: PRT
 ORGANISM: DROSOPHILA
 US-60-171-625-531

Query Match 100.0%; Score 29; DB 26; Length 634;
 Best Local Similarity 100.0%; Pred. No. 2.3e+03; Length 634;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEPRAS 6
 Db 26 LEPRAS 31

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using SW model.
Run on: June 6, 2002, 13:03:48 ; Search time 12.67 Seconds
(without alignments)
27.907 Million cell updates/sec

Title: US-09-627-383-1
Perfect score: 29
Sequence: 1 LEPRSS 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 186664 seqs, 58930901 residues
Total number of hits satisfying chosen parameters: 186664

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%, Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents AA New:
1: /cggn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:
2: /cggn2_6/ptodata/2/paa/US06_NEW_COMB.pep:
3: /cggn2_6/ptodata/2/paa/US07_NEW_COMB.pep:
4: /cggn2_6/ptodata/2/paa/US08_NEW_COMB.pep:
5: /cggn2_6/ptodata/2/paa/US09_NEW_COMB.pep:
6: /cggn2_6/ptodata/2/paa/US10_NEW_COMB.pep:
7: /cggn2_6/ptodata/2/paa/US60_NEW_COMB.pep:
;

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	26	89.7	61	5	US-09-540-209B-9237	Sequence 9237, APP
2	26	89.7	153	6	US-10-121-062-564	Sequence 564, APP
3	26	89.7	406	1	PCT-US2-11152-21	Sequence 21, APP
4	26	89.7	485	1	PCT-US02-11150-20	Sequence 20, APP
5	26	89.7	8360	6	US-10-132-134-34	Sequence 34, APP
6	25	86.2	24	1	PCT-US02-07282-6	Sequence 6, APP
7	25	86.2	24	6	US-10-114-500-6	Sequence 6, APP
8	25	86.2	58	5	US-09-859-604-538	Sequence 538, APP
9	25	86.2	177	6	US-10-113-872-1863	Sequence 1678, APP
10	25	86.2	214	5	US-09-540-209B-5669	Sequence 5669, APP
11	25	86.2	241	5	US-09-935-625-23288	Sequence 23288, APP
12	25	86.2	283	5	US-09-935-625-28	Sequence 28, APP
13	25	86.2	287	5	US-09-935-625-23287	Sequence 23287, APP
14	25	86.2	314	6	US-10-113-872-1863	Sequence 1863, APP
15	25	86.2	357	7	US-10-60-377-714-52	Sequence 52, APP
16	25	86.2	439	1	PCT-US02-07282-4	Sequence 4, APP
17	25	86.2	439	6	US-10-114-500-4	Sequence 4, APP
18	25	86.2	475	5	US-09-935-625-13383	Sequence 13383, APP
19	25	86.2	475	5	US-09-935-625-13383	Sequence 21538, APP
20	25	86.2	475	5	US-09-935-625-30024	Sequence 30024, APP
21	25	86.2	535	5	US-09-935-625-13382	Sequence 13382, APP
22	25	86.2	535	5	US-09-935-625-21537	Sequence 21537, APP
23	25	86.2	535	5	US-09-935-625-30023	Sequence 30023, APP
24	25	86.2	551	5	US-09-935-625-13165	Sequence 11615, APP
25	86.2	551	5	US-09-935-625-19542	Sequence 19542, APP	
551	86.2	551	5	US-09-935-625-28022	Sequence 28022, APP	

ALIGNMENTS

RESULT 1
US-09-540-209B-9237
; Sequence 9237, Application US/09540209B
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton
; TITLE OF INVENTION: FERULIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTERIOIDES
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709_1001-001
; CURRENT APPLICATION NUMBER: US/09/540, 209B
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 1044
; SEQ ID NO: 9237
; LENGTH: 61
; TYPE: PRT
; ORGANISM: B. fragilis
; US-09-540-209B-9237

Query Match 89.7%; Score 26; DB 5; Length 61;
Best Local Similarity 83.3%; Pred. No. 29;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEPRSS 6
Db 1 LEPRSS 6

RESULT 2
US-10-121-062-564
; Sequence 564, Application US/10121062
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Destroyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William L.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P34301C1
; CURRENT APPLICATION NUMBER: US/10/121, 062
; CURRENT FILING DATE: 2002-04-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612

```

; SEQ ID NO: 564
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-121-062-564

Query Match 89.7%; Score 26; DB 1; Length 153;
Best Local Similarity 83.3%; Pred. No. 2.3e+02; 0; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEPRAS 6
Db 145 LEPRAS 150

RESULT 3
PCT-US02-11152-21
Sequence 21, Application PC/US0211152
GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: AZIMZAI, Yalda
APPLICANT: AU-YOUNG, Janice K.
APPLICANT: BAKER, Sejeev
APPLICANT: BAUGH, Mariah R.
APPLICANT: BECHA, Shanya D.
APPLICANT: BOROWSKY, Mark L.
APPLICANT: BUFORD, Neil
APPLICANT: DING, Li
APPLICANT: ELLIOTT, Vicki S.
APPLICANT: EMERLING, Brooke M.
APPLICANT: GANDHI, Ameena R.
APPLICANT: GIEZEN, Kimberly J.
APPLICANT: GRIFFIN, Jennifer A.
APPLICANT: HAFALIA, April J.A.
APPLICANT: HONCHELL, Cynthia D.
APPLICANT: LAL, Preeti G.
APPLICANT: LEE, Soo Yeun
APPLICANT: LU, Duyng Aina M.
APPLICANT: ARVIZU, Chanda S.
APPLICANT: RAMKUMAR, Jayalaxmi
APPLICANT: REDDY, Roopa
APPLICANT: SANJANA, Madhu, M.
APPLICANT: TANG, Y. Tom
APPLICANT: WALIA, Narinder K.
APPLICANT: WARREN, Bridget A.
APPLICANT: XU, Yuming
APPLICANT: YAO, Monique G.
APPLICANT: YUE, Henry
APPLICANT: ZEBARJADIAN, Yeganeh
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL GROWTH, DIFFERENTIATION, AND DEATH
FILE REFERENCE: PI-0417 PCT
CURRENT APPLICATION NUMBER: PCT/US02/11152
CURRENT FILING DATE: 2002-04-05
PRIORITY APPLICATION NUMBER: 60/282,110; 60/283,294; 60/286,820; 60/287,228;
60/291,662; 60/291,846; 60/293,727; 60/295,340; 60/295,263; 60/349,705
PRIORITY FILING DATE: 2001-04-06; 2001-04-11; 2001-04-26; 2001-04-27;
2001-05-16; 2001-05-18; 2001-05-25; 2001-06-01; 2001-06-11; 2001-05-25; 2001-06-01; 2001-06-11; 2002-01-15
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PERL Program
SEQ ID NO: 21
LENGTH: 406
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE: misc_feature
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: 7506195CD1
PCT-US02-11152-21

```

```

Query Match 89.7%; Score 26; DB 1; Length 406;
Best Local Similarity 83.3%; Pred. No. 2.7e+02; 0; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEPRAS 6
Db 62 LQPRAS 67

RESULT 4
PCT-US02-11152-20
Sequence 20, Application PC/US0211152
GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: AZIMZAI, Yalda
APPLICANT: BAKER, Sejeev
APPLICANT: BAUGH, Mariah R.
APPLICANT: BECHA, Shanya D.
APPLICANT: BOROWSKY, Mark L.
APPLICANT: BUFORD, Neil
APPLICANT: DING, Li
APPLICANT: ELLIOTT, Vicki S.
APPLICANT: EMERLING, Brooke M.
APPLICANT: GANDHI, Ameena R.
APPLICANT: GIEZEN, Kimberly J.
APPLICANT: GRIFFIN, Jennifer A.
APPLICANT: HAFALIA, April J.A.
APPLICANT: HONCHELL, Cynthia D.
APPLICANT: LAL, Preeti G.
APPLICANT: LEE, Soo Yeun
APPLICANT: LU, Duyng Aina M.
APPLICANT: ARVIZU, Chanda S.
APPLICANT: RAMKUMAR, Jayalaxmi
APPLICANT: REDDY, Roopa
APPLICANT: SANJANA, Madhu, M.
APPLICANT: TANG, Y. Tom
APPLICANT: WALIA, Narinder K.
APPLICANT: WARREN, Bridget A.
APPLICANT: XU, Yuming
APPLICANT: YAO, Monique G.
APPLICANT: YUE, Henry
APPLICANT: ZEBARJADIAN, Yeganeh
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL GROWTH, DIFFERENTIATION, AND DEATH
FILE REFERENCE: PI-0417 PCT
CURRENT APPLICATION NUMBER: PCT/US02/11152
CURRENT FILING DATE: 2002-04-05
PRIORITY APPLICATION NUMBER: 60/282,110; 60/283,294; 60/286,820; 60/287,228;
60/291,662; 60/291,846; 60/293,727; 60/295,340; 60/295,263; 60/349,705
PRIORITY FILING DATE: 2001-04-06; 2001-04-11; 2001-04-26; 2001-04-27;
2001-05-16; 2001-05-18; 2001-05-25; 2001-06-01; 2001-06-11; 2002-01-15
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PERL Program
SEQ ID NO: 20
LENGTH: 485
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE: misc_feature
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: 4558650CD1
PCT-US02-11152-20

```

Db 62 LQPRAS 67
| : |||||

RESULT 5
US-10-132-134-34
; Sequence 34, Application US/10132134
; GENERAL INFORMATION:
; APPLICANT: Farnet, Chris
; APPLICANT: Yang, Xianshu
; APPLICANT: Staffa, Alfredo
; APPLICANT: Zazopoulos, Emmanuel
TITLE OF INVENTION: POLYKETIDE SYNTHASE ENZYMES
FILE REFERENCE: 3012-2US
CURRENT APPLICATION NUMBER: US/10/132,134
CURRENT FILING DATE: 2002-04-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn version 3.0
SEQ ID NO 34
LENGTH: 8360
TYPE: PRT
ORGANISM: Streptomyces amphibiosporus
US-10-132-134-34

Query Match 89.7%; Score 26; DB 6; Length 8360;
Best Local Similarity 83.3%; Pred. No. 5.8e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LEPRAS 6
||| : |||||

Db 6398 LEPRAA 6403
| : |||||
*RESULT 6
PCT-US02-07282-6
Sequence 6, Application PC/TUS0207/282
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; APPLICANT: Godbole, Shubhada D
; APPLICANT: Boyle, Bryan J
; APPLICANT: Arterburn, Matthew C
; APPLICANT: Liu, Chenghua
; APPLICANT: Tang, Y Tom
; APPLICANT: Drmanac, Radivoje T
; APPLICANT: Teng, Y Tom
; APPLICANT: Drmanac, Radivoje T
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO FIBULIN-LIKE POLYPEPTIDES AND
TITLE OF INVENTION: POLYNUCLEOTIDES
FILE REFERENCE: 24059-000-061
CURRENT APPLICATION NUMBER: PCT/US02/07282
CURRENT FILING DATE: 2002-03-08
PRIOR APPLICATION NUMBER: US 09/802,704
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: US 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/496,914
PRIOR FILING DATE: 2000-02-03
SEQ ID NO 6
LENGTH: 24
TYPE: PRT
ORGANISM: Homo sapiens
US-10-132-134-34

Query Match 89.7%; Score 26; DB 6; Length 8360;
Best Local Similarity 83.3%; Pred. No. 5.8e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LEPRAS 6
||| : |||||
Db 6398 LEPRAA 6403
| : |||||

*RESULT 7
PCT-US02-07282-6
Sequence 6, Application PC/TUS0207/282
; GENERAL INFORMATION:
; APPLICANT: Godbole, Shubhada D
; APPLICANT: Boyle, Bryan J
; APPLICANT: Arterburn, Matthew C
; APPLICANT: Liu, Chenghua
; APPLICANT: Drmanac, Radivoje T
; APPLICANT: Tang, Y Tom
; APPLICANT: Drmanac, Radivoje T
; APPLICANT: Teng, Y Tom
; APPLICANT: Drmanac, Radivoje T
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO FIBULIN-LIKE POLYPEPTIDES AND
TITLE OF INVENTION: POLYNUCLEOTIDES
FILE REFERENCE: 24059-000-061
CURRENT APPLICATION NUMBER: PCT/US02/07282
CURRENT FILING DATE: 2002-03-08
PRIOR APPLICATION NUMBER: US 09/802,704
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: US 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/496,914
PRIOR FILING DATE: 2000-02-03
SEQ ID NO 6
LENGTH: 24
TYPE: PRT
ORGANISM: Homo sapiens
US-10-132-134-34

Query Match 86.2%; Score 25; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 EPRAS 6
||| : |||||
Db 20 EPRAS 24
| : |||||

Query Match 86.2%; Score 25; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 EPRAS 6
||| : |||||
Db 20 EPRAS 24
| : |||||
PCT-US02-07282-6
| : |||||
*RESULT 8
US-09-855-604-538
Sequence 538, Application US/09855604
; GENERAL INFORMATION:
; APPLICANT: Gicolel, Brigitte
; APPLICANT: Poronoi, Denis
; APPLICANT: Lim, Eng-Mong
; APPLICANT: Pelicic, Vladimir
; APPLICANT: Gutuenco, Agnes
; APPLICANT: Goguet, De La Salmoniere, Yves
TITLE OF INVENTION: POLYPEPTIDE NUCLEIC SEQUENCES EXPORTED FROM MYCOBACTERIA,
TITLE OF INVENTION: VECTORS COMPRISING SAME AND USES FOR DIAGNOSING AND
TITLE OF INVENTION: PREVENTING TUBERCULOSIS
FILE REFERENCE: 03715.0052-01000
CURRENT APPLICATION NUMBER: US/09/855,604
CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 09/485,536
PRIOR FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: PCT/FR98/01813
PRIOR FILING DATE: 1998-08-14
PRIOR APPLICATION NUMBER: FR 97 10404
PRIOR FILING DATE: 1997-06-14
PRIOR APPLICATION NUMBER: FR 97 11325
PRIOR FILING DATE: 1997-09-11
NUMBER OF SEQ ID NOS: 935
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 538
LENGTH: 58
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
US-09-855-604-538

Query Match Similarity 86.2%; Score 25; DB 5; Length 58;
 Best Local Similarity 100.0%; Pred. No. 47; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	2 EPRAS 6	Db	4 EPRAS 8

RESULT 9
 US-10-113-872-1678
 ; Sequence 1678, Application US/10113872
 ; GENERAL INFORMATION:
 ; APPLICANT: Watanabe, Yoshihiro
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Sleath, Paul R.
 ; APPLICANT: Vedvick, Thomas S.
 ; APPLICANT: Carter, Barrick
 ; APPLICANT: Fanger, Gary R.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
 ; FILE REFERENCE: 210121-478C19
 ; CURRENT APPLICATION NUMBER: US/10/113,872
 ; CURRENT FILING DATE: 2002-03-28
 ; NUMBER OF SEQ ID NOS: 2011
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 1678
 ; LENGTH: 177
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-113-872-1678

Query Match Similarity 86.2%; Score 25; DB 6; Length 177;
 Best Local Similarity 100.0%; Pred. No. 1.6e-02; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	2 EPRAS 6	Db	20 EPRAS 24

RESULT 10
 US-09-540-209B-5669
 ; Sequence 5669, Application US/09540209B
 ; GENERAL INFORMATION:
 ; APPLICANT: Gary L. Breton
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES FR
 ; FILE REFERENCE: 2709-1001-001
 ; CURRENT APPLICATION NUMBER: US/09/540,209B
 ; CURRENT FILING DATE: 2000-04-04
 ; NUMBER OF SEQ ID NOS: 10444
 ; SEQ ID NO 5669
 ; LENGTH: 214
 ; TYPE: PRT
 ; ORGANISM: B fragilis
 ; US-09-540-209B-5669

Query Match Similarity 86.2%; Score 25; DB 5; Length 214;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 LEPRAS 5	Db	4 LEPRAS 8

RESULT 11
 US-09-933-625-23288
 ; Sequence 23288, Application US/099335625

Query Match Similarity 86.2%; Score 25; DB 5; Length 58;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 LEPRAS 5	Db	97 LEPRAS 101

RESULT 12
 US-09-895-913A-28
 ; Sequence 28, Application US/09895913A
 ; GENERAL INFORMATION:
 ; APPLICANT: Kleanthous, Harold
 ; APPLICANT: Al-Garawi, Amal
 ; APPLICANT: Miller, Charles
 ; APPLICANT: Tomb, Jean Francois
 ; APPLICANT: Omen, Raymond P.
 ; TITLE OF INVENTION: Identification of Polynucleotides
 ; TITLE OF INVENTION: Encoding Novel Helicobacter Polypeptides in the Helicobacter
 ; FILE REFERENCE: 06132/043002
 ; CURRENT APPLICATION NUMBER: US/09/895,913A
 ; CURRENT FILING DATE: 2001-06-29
 ; PRIOR APPLICATION NUMBER: US 08/881,227
 ; PRIOR FILING DATE: 1997-06-24
 ; NUMBER OF SEQ ID NOS: 368
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 28
 ; LENGTH: 283
 ; TYPE: PRT
 ; ORGANISM: Helicobacter pylori
 ; US-09-895-913A-28

Query Match Similarity 86.2%; Score 25; DB 5; Length 283;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 LEPRAS 5	Db	140 LEPRAS 144

RESULT 13
 US-09-935-625-23287
 ; Sequence 23287, Application US/09935625
 ; GENERAL INFORMATION:
 ; APPLICANT: N. ALEXANDROV et al.
 ; TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, CELLS, AND METHODS THEREOF CAPA
 ; TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, CELLS, AND METHODS THEREOF CAPA
 ; FILE REFERENCE: 2750-1481P
 ; CURRENT APPLICATION NUMBER: US/09/935,625
 ; CURRENT FILING DATE: 2001-08-24

NUMBER OF SEQ ID NOS: 33136
 SEQ ID NO 23287
 LENGTH: 287
 TYPE: PRY
 ORGANISM: Arabidopsis thaliana
 FEATURE: peptide
 NAME/KEY: peptide
 LOCATION: 1..287
 OTHER INFORMATION: Ceres Seq. ID no. 2028608
 US-09-935-625-23287

Query Match 86.2%; Score 25; DB 5; Length 287;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;
 QY 1 LEPRA 5
 Db 123 LEPRA 127

Query Match 86.2%; Score 25; DB 7; Length 367;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;
 QY 1 LEPRA 5
 Db 132 LEPRA 136

Search completed: June 6, 2002, 13:04:51
 Job time: 63 sec

RESULT 14
 US-10-113-872-1863
 ; Sequence 1863, Application US/10113872
 GENERAL INFORMATION:
 APPLICANT: Watanabe, Yoshihiro
 APPLICANT: Henderson, Robert A.
 APPLICANT: Kalos, Michael D.
 APPLICANT: Sleath, Paul R.
 APPLICANT: Vedick, Thomas S.
 APPLICANT: Carter, Darrick
 APPLICANT: Ranger, Gary R.
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
 FILE REFERENCE: 210121.478C19
 CURRENT FILING DATE: 2002-03-28
 NUMBER OF SEQ ID NOS: 2011
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 1863
 LENGTH: 314
 TYPE: PRY
 ORGANISM: Homo sapiens
 US-10-113-872-1863

Query Match 86.2%; Score 25; DB 6; Length 314;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;

QY 2 EPPRS 6
 Db 157 EPPRS 161

RESULT 15
 US-60-377-714-52

; Sequence 52, Application US/60377714
 GENERAL INFORMATION:
 APPLICANT: Ward, Teresa R
 APPLICANT: Mao, Mao
 APPLICANT: Linsley, Peter S
 FILE REFERENCE: R02-016-200
 CURRENT APPLICATION NUMBER: US/60/377,714
 CURRENT FILING DATE: 2002-05-03
 NUMBER OF SEQ ID NOS: 111
 SOFTWARE: PatentIn Version 3.1
 SEQ ID NO 52
 LENGTH: 367
 TYPE: PRY
 ORGANISM: Homo sapiens
 US-60-377-714-52

Thu Jun 6 15:17:16 2002

us-09-627-383-1.rapn

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model
Run on: June 6, 2002, 13:03:48 ; Search time 30 Seconds
(without alignments)

22.215 Million cell updates/sec
Title: US-09-627-383-1
Perfect score: 29
Sequence: 1 LEPRAS 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 747574 seqs, 111073196 residues
Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_032802:*

1: /SIDS1/gcdata/hold-geneseq/geneseqp-emb1/AA1980.DAT:*

2: /SIDS1/gcdata/hold-geneseq/geneseqp-emb1/AA1981.DAT:*

3: /SIDS1/gcdata/hold-geneseq/geneseqp-emb1/AA1982.DAT:*

4: /SIDS1/gcdata/hold-geneseq/geneseqp-emb1/AA1983.DAT:*

5: /SIDS1/gcdata/hold-geneseq/geneseqp-emb1/AA1984.DAT:*

6: /SIDS1/gcdata/hold-geneseq/geneseqp-emb1/AA1985.DAT:*

7: /SIDS1/gcdata/hold-geneseq/geneseqp-emb1/AA1986.DAT:*

8: /SIDS1/gcdata/hold-geneseq/geneseqp-emb1/AA1987.DAT:*

9: /SIDS1/gcdata/hold-geneseq/geneseqp-emb1/AA1988.DAT:*

10: /SIDS1/gcdata/hold-geneseq/geneseqp-emb1/AA1989.DAT:*

11: /SIDS1/gcdata/hold-geneseq/geneseqp-emb1/AA1990.DAT:*

12: /SIDS1/gcdata/hold-geneseq/geneseqp-emb1/AA1991.DAT:*

13: /SIDS1/gcdata/hold-geneseq/geneseqp-emb1/AA1992.DAT:*

14: /SIDS1/gcdata/hold-geneseq/geneseqp-emb1/AA1993.DAT:*

15: /SIDS1/gcdata/hold-geneseq/geneseqp-emb1/AA1994.DAT:*

16: /SIDS1/gcdata/hold-geneseq/geneseqp-emb1/AA1995.DAT:*

17: /SIDS1/gcdata/hold-geneseq/geneseqp-emb1/AA1996.DAT:*

18: /SIDS1/gcdata/hold-geneseq/geneseqp-emb1/AA1997.DAT:*

19: /SIDS1/gcdata/hold-geneseq/geneseqp-emb1/AA1998.DAT:*

20: /SIDS1/gcdata/hold-geneseq/geneseqp-emb1/AA2000.DAT:*

21: /SIDS1/gcdata/hold-geneseq/geneseqp-emb1/AA2001.DAT:*

22: /SIDS1/gcdata/hold-geneseq/geneseqp-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID

ALIGNMENTS			
RESULT	1		
ID	AAB0246	AAB0246 standard; peptide; 6 AA.	XX
AC	AAB0246;		XX
DT	04-MAY-2001	(first entry)	XX
DE	Peptide for identifying fluorescent insensitive sites in GFP.		
XX	Affinity fluorescent protein; detection; reporter.		
KW	Synthetic.		
OS			
PN	WO20109177-A2.		XX
XX			
PF	28-JUL-2000; 2000WO-US20619.		XX
XX			
PR	29-JUL-1999; 99US-0146438.		XX
XX			
PA	(WHED) WHITEHEAD INST BIOMEDICAL RES.		
XX			
PI	Matsudaira PT, Ehrlich DJ, Zhong Q, Freyson Y;		
XX			
DR	WPI: 2001-159952/16.		
XX			
PT	New affinity fluorescent protein comprising a modified fluorescent protein having a heterologous amino acid sequence and a ligand-activated protein binding site, for detecting target ligand in a mixture of macromolecules or in a cell		
PT			
XX			
PS	Claim 12; Page 8; 44pp; English.		

12	29	100.0	1077	22	ABB61324
13	29	100.0	1219	21	AYAY8795
14	29	100.0	2359	22	ABA65476
15	29	100.0	2548	20	AY05781
16	29	100.0	3096	22	ABA6770
17	27	93.1	147	20	AYT7779
18	26	89.7	21	AYT0693	
19	26	89.7	18	AYY0366	
20	26	89.7	30	ABB1870	
21	26	89.7	30	AA005368	
22	26	89.7	31	AA00930	
23	26	89.7	32	AAU7436	
24	26	89.7	32	AAO1760	
25	26	89.7	33	AAO10563	
26	26	89.7	34	AAU09091	
27	26	89.7	35	AA005223	
28	26	89.7	35	AA013356	
29	26	89.7	39	AAW19897	
30	26	89.7	39	AAU13753	
31	26	89.7	40	AAU07978	
32	26	89.7	42	AAU1189	
33	26	89.7	42	AAU13356	
34	26	89.7	43	AAW06431	
35	26	89.7	43	AAU06431	
36	25	89.7	43	AAU1676	
37	26	89.7	43	AAU1697	
38	26	89.7	43	AAU12990	
39	25	89.7	44	AAU1548	
40	26	89.7	45	AAU01116	
41	26	89.7	46	AAU01664	
42	26	89.7	46	AAU11996	
43	26	89.7	47	AAU13529	
44	26	89.7	47	AAU13774	
45	26	89.7	48	AAU96064	

xx The present invention relates to an affinity fluorescent protein
 cc (aFP), having a modified fluorescent protein molecule with a mutated
 cc fluorescent protein molecule and a heterologous amino acid sequence
 cc with a ligand-activatable protein binding site. The invention is useful
 cc for detecting target ligands in a mixture of macromolecules or a cell,
 cc for detecting and monitoring a range of biological activities and as
 cc a substitute for reporter-molecule labeled monoclonal or
 cc polyclonal antibodies.

xx Sequence 6 AA:

Query Match Similarity 100.0%; Score 29; DB 22; Length 6;
 Best Local Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEPRAS 6
 Db 1 lepras 6

RESULT 2

ID AAU31081 standard; Protein; 119 AA.

XX AAU31081; AC
 XX AAU31081; DT 18-DEC-2001 (first entry)

XX DE Novel human secreted protein #1572.

DE Human: vaccination; gene therapy; nutritional supplement;
 KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
 KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
 OS Homo sapiens.

XX WO200179449-A2.

PN XX 25-OCT-2001.

PD XX 16-APR-2001; 2001WO-US08656.

PF XX 18-APR-2000; 2000US-0552929.

PR XX 26-JAN-2001; 2001US-0770160.

PA XX (HYSE-) NYSEQ INC.

XX PI Tang YT, Liu C, Dumanac RT;
 XX DR WPI; 2001-611725/70.

PT Nucleic acids encoding a range of human polypeptides, useful in genetic
 vaccination, testing and therapy -

XX PS Claim 20; Page 400; 765pp; English.

XX The invention relates to novel human secreted polypeptides. The
 cc polypeptides and antibodies to the polypeptides are useful for
 cc determining the presence of or predisposition to a disease associated
 cc with altered levels of polypeptide. The polypeptides are also useful for
 cc identifying agents (agonists and antagonists) that bind to them. Cells
 cc expressing the proteins are useful for identifying a therapeutic agent
 cc for use in treatment of a pathology related to aberrant expression or
 cc physiological interactions of the polypeptide. Vectors comprising
 cc the nucleic acids encoding the polypeptides and cells genetically
 cc engineered to express them are also useful for producing the proteins.
 cc The proteins are useful in genetic vaccination, testing and
 cc therapy, and can be used as nutritional supplements. They may be used to
 cc increase stem cell proliferation; to regulate haematopoiesis; and in
 cc bone, cartilage, tendon and/or nerve tissue growth or regeneration;
 cc immune suppression and/or stimulation; as anti-inflammatory agents; and
 cc

cc in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid
 cc sequences of novel human secreted proteins of the invention.

xx Sequence 119 AA:

Query Match Similarity 100.0%; Score 29; DB 22; Length 119;
 Best Local Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEPRAS 6
 Db 81 lepras 86

RESULT 3

ID AAU39701 standard; Protein; 125 AA.

XX AAU39701; AC
 XX AAU39701; DT 13-FEB-2002 (first entry)

XX DE Propionibacterium acnes immunogenic protein #597.

XX PR 01-NOV-2001.

PD XX 20-APR-2001; 2001WO-US12865.

PF XX 21-APR-2000; 2000US-199647P.
 PR 02-JUN-2000; 2000US-20881P.
 PR 07-JUL-2000; 2000US-216747P.

PA XX (CORI-) CORIXA CORP.

XX PI Skeley YAN, Persing DH, Mitcham JL, Wang SS, Bhatia A;
 PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
 XX DR WPI; 2001-616774/71.
 DR N-PSDB; AAS59508.

XX PT Propionibacterium acnes polypeptides and nucleic acids useful for
 PT vaccinating against and diagnosing infections, especially useful for
 PT treating acne vulgaris -

XX PS Example 1; SEQ ID No 896, 1069pp; English.

XX Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
 cc polypeptides. The proteins and their associated DNA sequences are used in
 cc the treatment, prevention and diagnosis of medical conditions caused by
 cc P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
 cc pustulosis, hypertrichosis and osteomyelitis), urethritis and endophthalmitis.
 cc P. acnes is also involved in infections of bone, joints and the central
 cc nervous system, however it is particularly involved in the inflammatory
 cc lesions associated with acne vulgaris. A method for detecting the
 cc presence or absence of P. acnes in a patient comprises contacting a
 cc sample with a binding agent that binds to the proteins of the invention
 cc and determining the amount of bound protein in the sample. The
 cc polypeptides may be used as antigens in the production of antibodies
 cc specific for P. acnes proteins. These antibodies can be used to
 cc downregulate expression and activity of P. acnes polypeptides and
 cc therefore treat P. acnes infections. The antibodies may also be used as
 cc diagnostic agents for determining P. acnes presence, for example, by
 cc enzyme linked immunosorbent assay (ELISA).

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp://wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences).

```

Query Match          100.0%;  Score 29;  DB 22;  Length 125;
Best Local Similarity 100.0%;  pred. No. 92;
Matches      6;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0
> 1 LEPHAS 6
> 85 lepras 90

```

Matches	6;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Oy	1	LEPRAS	6						
Db	146	lepras	151						
RESULT	5								
AAB93466									
ID	RAB93466	standard;	protein:	526	AA.				
XX									
AC	AAB93466;								
XX									
DT	26-JUN-2001	(first entry)							
XX									
DE	Human	protein	sequence	SEQ	ID	NO:12736.			

WPI; 1999-095324/08.

New mammalian Zneul polypeptides - used to, e.g. treat Alzheimer's disease, cancer and to repopulate blood cells

Claim 6: Page 54; 70pp; English.

This polypeptide comprises a novel mammalian Zneul polypeptide. Novel human Zneul (see AAW88381) is a new neuro-growth factor-like protein that shows homology to Notch 4 and which may be involved in EGFR receptor pathways. Zneul can be used as a growth, maintenance, or differentiator factor in the spinal cord, heart, spleen, testis, thyroid and lymph nodes. It may also be used to treat Alzheimer's disease, cancer, to repopulate blood cells after chemotherapy, to stimulate myofibroblast proliferation, stimulate or inhibit growth factors made in the placenta, in fertility and contraception, or to regenerate nerves. Claimed Zneul polypeptides (see also AAW88322-97), including specific domains of Zneul and epitope-bearing portions of Zneul, can be used to raise specific antibodies for use e.g. in diagnostic assays.

Sequence

256 AA:

AC AAW88383;
 XX
 DT 26-APR-1999 (first entry)
 XX
 DE Mammalian Zneul polypeptide.
 XX
 KW Zneu-1; neuro-growth factor-like protein; human; breast cancer;
 KW glioblastoma; pituitary adenoma; Alzheimer's disease; therapy;
 KW nerve regeneration; haematopoiesis; fertility; contraception;
 KW antibody.
 XX
 OS Class - Mammalia.
 XX
 WO9857983-A2.
 XX
 PD 23-DEC-1998.
 XX
 PR 18-JUN-1998; 98WO-US12763.
 XX
 PR 18-JUN-1997; 97US-0878322.
 PR 18-JUN-1997; 97US-0050143.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Blumberg H, Jelinek LJ, Lehner JM, Sheppard PO;
 PI Whitmore TE;
 XX
 DR WPI; 1999-095324/08.
 XX
 PT New mammalian Zneul polypeptides - used to, e.g. treat Alzheimer's
 PT disease, cancer and to repopulate blood cells
 XX
 PS Claim 6; Page 51-53; 70pp; English.
 XX
 CC This polypeptide comprises a novel mammalian Zneul polypeptide.
 CC Novel human Zneul (see AAW88381) is a new neuro-growth factor-like
 CC protein that shows homology to Notch 4 and which may be involved in
 CC EGF receptor pathways. Zneul can be used as a growth, maintenance,
 CC or differentiation factor in the spinal cord, heart, spleen,
 CC testis, thyroid and lymph nodes. It may also be used to treat
 CC Alzheimer's disease, cancer, to repopulate blood cells after
 CC chemotherapy, to stimulate myoblast proliferation, stimulate
 CC or inhibit growth factors made in the placenta, in fertility and
 CC contraction, or to regenerate nerves. Claimed Zneul polypeptides
 (see also AAW88382-97), including specific domains of Zneul and
 CC epitope-bearing portions of Zneul, can be used to raise specific
 CC antibodies for use e.g. in diagnostic assays.
 XX
 SQ Sequence 708 AA;

Query Match 100.0%; Score 29; DB 20; length 708;
 Best Local Similarity 100.0%; Pred. No. 5.1e-02; Mismatches 0; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEPRAS 6
 ID AAM38679
 AC AAM38679;
 XX
 DT 22-OCT-2001 (first entry)
 XX
 DE Human polypeptide SEQ ID NO 1824.

KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;

AC AAI57798-AAI61369;
 XX
 PS Example 3; SEQ ID NO 1824; 10078pp; English.
 XX
 CC The invention relates to human nucleic acids (AAI57798-AAI61369), and
 CC the encoded polypeptides (AM36642-AM4213), with nootropic,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: Immune system suppression,
 CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemias and
 CC C.N.S disorders.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification.
 XX
 SQ Sequence 966 AA;

Query Match 100.0%; Score 29; DB 22; Length 966;
 Best Local Similarity 100.0%; Pred. No. 6.9e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEPRAS 6
 ID AAM38678
 AC AAM38678;
 XX
 DT 22-OCT-2001 (first entry)
 XX
 DE Human polypeptide SEQ ID NO 1823.

XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW anvotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 leukaemia.
 XX Homo sapiens.
 PN WO200153312-A1.
 XX PD 26-JUL-2001.
 XX PF 26-DEC-2000; 2000WO-US34263.
 XX PR 21-JAN-2000; 2000US-0488725.
 PR 25-APR-2000; 2000US-052317.
 PR 09-JUL-2000; 2000US-058042.
 PR 19-JUL-2000; 2000US-0620312.
 PR 01-AUG-2000; 2000US-053450.
 PR 14-SEP-2000; 2000US-066191.
 PR 19-OCT-2000; 2000US-0623036.
 PR 29-NOV-2000; 2000US-0727344.
 PA (HYSE-) HYSEQ INC.
 XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
 PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
 XX DR WPI; 2001-442253/47.
 PT Novel nucleic acids and polypeptides, useful for treating disorders
 such as central nervous system injuries -
 XX PS Example 3; SEQ ID NO 1823; 10078pp; English.

The invention relates to human nucleic acids (AAT57798-AA161369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, anvotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form part of the printed specification.

XX Sequence 1013 AA;

Query Match 100.0%; Score 29; DB 22; Length 1013;

Best Local Similarity 100.0%; Pred. No. 7.2e+02; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEPRSS 6
 Db 147 lepras 152

XX 22-OCT-2001 (first entry).
 DT XX Human polypeptide SEQ ID NO 1825.
 DE XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW anvotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 leukaemia.
 XX Homo sapiens.
 PN WO200153312-A1.
 XX PD 26-JUL-2001.
 XX PF 26-DEC-2000; 2000WO-US34263.
 XX PR 21-JAN-2000; 2000US-0488725.
 PR 25-APR-2000; 2000US-052317.
 PR 09-JUL-2000; 2000US-058042.
 PR 19-JUL-2000; 2000US-0620312.
 PR 03-AUG-2000; 2000US-062191.
 PR 14-SEP-2000; 2000US-0633450.
 PR 19-OCT-2000; 2000US-0633036.
 PR 29-NOV-2000; 2000US-0727344.
 PA (HYSE-) HYSEQ INC.
 XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
 PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
 XX DR WPI; 2001-442253/47.
 PT Novel nucleic acids and polypeptides, useful for treating disorders
 such as central nervous system injuries -
 XX PS Example 3; SEQ ID NO 1825; 10078pp; English.

The invention relates to human nucleic acids (AAT57798-AA161369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, anvotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form part of the printed specification.

XX Sequence 1025 AA;

Query Match 100.0%; Score 29; DB 22; Length 1025;

Best Local Similarity 100.0%; Pred. No. 7.3e+02; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEPRSS 6
 Db 147 lepras 152

RESULT 11
 AAM38680
 ID AAM38680 standard; Protein; 1025 AA.
 XX AAM38680;
 AC

RESULT 12

ABB61324
 ID ABB61324 standard; Protein; 1077 AA.
 XX
 AC
 XX
 ABB61324;
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster polypeptide SEQ ID NO 10764.
 XX
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 OS Drosophila melanogaster.
 XX
 PN WO200171042-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 23-MAR-2001; 2001WO-US09231.
 XX
 PR 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX
 PA (PEKE) PE CORP NY.
 XX
 PI Venter JC, Adams M, Li PWD, Myers EW;
 XX
 WPI; 2001-656860/75.
 DR N-PSDB; ABL05427.
 DR
 PR New isolated nucleic acid detection reagent for detecting 1000 or more
 genes from Drosophila and for elucidating cell signalling and cell-cell
 interactions -
 PT Disclosure; SEQ ID NO 10764; 21pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 capable of detecting 1000 or more genes from Drosophila. The invention is
 useful in developmental biology and in elucidating cell signalling and
 cell-cell interactions in higher eukaryotes for the development of
 insecticides, therapeutics and pharmaceutical drugs. The invention
 discloses genomic DNA sequences (ABL01840-ABL16175) expressed DNA
 sequences (ABL01840-ABL16175) and the encoded proteins
 (ABB57737 ABB72072).
 CC The sequence data for this patent did not form part of the printed
 specification, but was obtained in electronic format directly from WIPO
 CC at ftp://wipo.int/pub/published/pct_sequences.
 XX
 SQ Sequence 1077 AA;

Query Match 100.0%; Score 29; DB 22; Length 1077;
 Best Local Similarity 100.0%; Pred. No. 7.6e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEPRAS 6
 Db 828 lepras 833

RESULT 13
 AAY78795 AAY78795 standard; Protein; 1219 AA.
 XX
 AC AAY78795;
 XX
 DT 19-MAY-2000 (first entry)
 XX
 DE Human antizui-2 (AZ-2) amino acid sequence.
 XX
 KW Antizui-2; AZ-2; human; breast cancer; malignancy progression marker;
 KW malignancy reversion; tumour suppressor.
 XX

OS Homo sapiens.
 XX
 PN WO200000503-A1.
 XX
 PD 06-JAN-2000.
 XX
 PR 25-JUN-1999; 99WO-US14482.
 XX
 PR 26-JUN-1998; 98US-0090747.
 XX
 PA (CHEN/) CHEN H.
 PA (BTSS/) BISSELL M.
 XX
 PI Chen H, Bissell M;
 XX
 WPI; 2000-170903/15.
 DR N-PSDB; AAZ90112.
 DR
 PS Claim 6; Page 69-72; 120pp; English.
 XX
 CC This sequence represents the human antizui-2 (AZ-2) amino acid
 sequence. The AZ-2 gene is a variant of the antizui-1 (AZ-1) gene (see
 AAZ90111). The AZ-1 gene is located on chromosome 10q26 and encodes a
 protein that acts as a tumour suppressor or marker of malignancy
 progression or reversion. The AZ-1 protein and its variants are tumour
 suppressors. AZ-1 interacts with E-cadherin and beta-catenin. Detecting
 low levels of AZ-1 nucleotide or amino acid sequences are used to
 diagnose a breast cell malignancy, also for monitoring disease
 progression, particularly assessment of therapeutic efficacy. The
 nucleotide sequence is used in in vivo or ex vivo gene therapy, and AZ-1
 polypeptides are used for treating or preventing breast cancer. AZ-1
 polypeptides are also used to raise specific antibodies, for diagnostic
 detection of AZ-1. Fragments of the AZ-1 nucleotide sequence are useful
 as probes or primers for detecting expression of the AZ-1 gene.
 CC Sequence 1219 AA;

Query Match 100.0%; Score 29; DB 21; Length 1219;
 Best Local Similarity 100.0%; Pred. No. 8.6e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEPRAS 6
 Db 404 lepras 409

RESULT 14
 AAB66476 AAB66476 standard; Protein; 2359 AA.
 XX
 ID AAB66476 standard; Protein; 2359 AA.
 XX
 AC AAB66476;
 XX
 DT 09-APR-2001 (first entry)
 XX
 DE Rat alpha-1H calcium channel protein.
 XX
 DE Rat alpha-1H calcium channel protein.
 XX
 DE Rat; expressed sequence tag; EST; antiarrhythmic; anticonvulsant;
 KW hypotensive; cardiotonic; β -type calcium channel subunit;
 KW cardiac hypertrophy; cardiac arrhythmia; hypertension; sleep disorder;
 KW epilepsy; alpha-1H calcium channel.
 XX
 OS Rattus sp.
 XX
 PN WO200102561-A2.
 XX
 PD 11-JAN-2001.
 XX
 PF 04-JUL-2000; 2000WO-CA00794.

FT	Domain	2074..2219	/note= "GAP domain, specifically claimed in Claim 3g"
PR			
XX			
PA			
(NEUR-) NEUROMED TECHNOLOGIES INC.			
PI			
XX			
Snutch TP, Baillie DL;			
DR			
WPI; 2001-123111/13.			
DR			
N-PSDB; AAF31678.			
XX			
PT			
Novel T-type calcium channel alpha-1 subunit gene useful for treating			
cardiac hypertrophy, cardiac arrhythmia, hypertension, sleep disorder			
and epilepsy -			
PT			
XX			
PS			
Disclosure; Page 75-85; 103pp; English.			
XX			
CC			
The present sequence is given in a specification providing sequences			
and partial sequences for three types of mammalian (human and rat)			
T-type calcium channel subunits. An expression cassette has been			
generated which comprises a nucleotide sequence encoding a T-type			
calcium channel alpha-1 subunit operably linked to control sequences			
to effect its expression. The novel calcium channel nucleic acids and			
proteins are useful for treating conditions characterised by			
undesirable levels of T-type calcium channel activity such as cardiac			
hypertrophy, cardiac arrhythmia, hypertension, sleep disorder and			
epilepsy.			
CC			
CC			
CC			
XX			
SQ			
Sequence 2359 AA;			
XX			
Query Match 100.0%; Score 29; DB 22; Length 2359;			
Best Local Similarity 100.0%; Pred. No. 1.7e+03;			
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY 1 LEPRAS 6			
Db 1968 lepras 1973			
RESULT 15			
AY05781 AAY05781 standard; Protein; 2548 AA.			
ID AAY05781;			
XX			
AC			
Db 1968 lepras 1973			
02-AUG-1999 (first entry)			
SQ			
Human myosin Ixa.			
DE			
XX			
KW Myosin Ixa; human; Bardet-Biedl syndrome; Usher syndrome; diagnosis;			
KW therapy; hearing loss; deafness; retinitis pigmentosa; obesity;			
KW hypogonadism; sterility; polydactyly; brachydactyly; syndactyly;			
KW mental retardation; renal abnormality; kidney disease;			
KW hypertension; diabetes; cardiovascular abnormality.			
XX			
OS Homo sapiens.			
XX			
Key Location/Qualifiers			
FH Region 1..146			
FT /note= "N-terminal extension, specifically claimed			
FT /note= "in claim 3b"			
FT Domain 147..719			
FT /note= "head domain, specifically claimed in Claim			
FT 3c"			
FT Binding-site 239..246			
FT /note= "ATP binding loop, specifically claimed in			
FT Claim 3d"			
FT Region 720..835			
FT /note= "minimal length 2nd insert, specifically			
FT 972..1166			
FT /note= "light chain binding domain, specifically			
FT claimed in Claim 3f"			
FT claimed in Claim 3d"			
XX			
Search completed: June 6, 2002, 13:05:28			
Job time: 100 sec			

Thu Jun 6 15:17:13 2002

us-09-627-383-1.rag

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

Om protein - protein search, using sw model

Run on: June 6, 2002, 13:03:48 ; Search time 12.96 Seconds
(without alignments)
11.308 Million cell updates/sec

Title: US-09-627-383-1
Perfect score: 29
Sequence: 1 LEPRA 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*

1: /cgn2_6/patdata/2/iaa/5A_COMB_pep:*

2: /cgn2_6/patdata/2/iaa/5B_COMB_pep:*

3: /cgn2_6/patdata/2/iaa/6A_COMB_pep:*

4: /cgn2_6/patdata/2/iaa/6B_COMB_pep:*

5: /cgn2_6/patdata/2/iaa/PCWUS_COMB_pep:*

6: /cgn2_6/patdata/2/iaa/bacfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	29	100.0	1261	1 US-08-764-100-26
2	29	100.0	1385	2 US-08-687-390-7
3	29	100.0	2548	4 US-09-172-422-1
4	29	100.0	2887	4 US-08-462-467B-2
5	29	100.0	2887	4 US-08-462-467B-8
6	29	100.0	3218	1 US-08-764-100-27
7	26	89.7	43	2 US-08-652-816A-43
8	26	89.7	1788	2 US-08-962-284-2
9	26	89.7	7257	3 US-09-335-409-5
10	26	89.7	7257	4 US-09-568-480-5
11	26	89.7	7257	4 US-09-568-480-5
12	26	89.7	7257	4 US-09-568-486-5
13	26	89.7	7257	4 US-09-568-472-5
14	26	89.7	7257	4 US-09-568-472-5
15	25	86.2	102	2 US-08-808-982-8
16	25	86.2	102	4 US-09-568-480A-8
17	25	86.2	118	4 US-09-567-965-5
18	25	86.2	159	3 US-08-390-333A-5
19	25	86.2	221	3 US-08-390-333A-6
20	25	86.2	297	1 US-07-866-590-6
21	25	86.2	297	1 US-08-077-673-6
22	25	86.2	297	1 US-08-077-692-6
23	25	86.2	297	3 US-09-105-298-6
24	25	86.2	297	3 US-08-06-288A-10
25	25	86.2	297	4 US-09-097-231-10
26	25	86.2	413	3 US-08-90-353A-7
27	25	86.2	413	3 US-08-390-353A-1

ALIGNMENTS

RESULT 1
US-08-764-100-26
Sequence 26, Application US/08764100
; Patent No. 5773700
GENERAL INFORMATION:
APPLICANT: van Grinsven J., Martinus Q.
APPLICANT: De Haan, Petrus T.
APPLICANT: Gieelen L., Johannes J.
APPLICANT: Peters, Birk
APPLICANT: Goldbach, Robert W.
TITLE OF INVENTION: Improvements in or Relating to Organic Compounds
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sandoz Agro, Inc
STREET: 975 California Avenue
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,100
FILING DATE: 06-DEC-1996
CLASSIFICATION: 800
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/08/214,064
FILING DATE:
APPLICATION NUMBER: US 08/032,235
FILING DATE: 17-MAR-1993
APPLICATION NUMBER: GB 9206016.9
FILING DATE: 19-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5773001s, Allen E.
REGISTRATION NUMBER: 34,490
REFERENCE/DOCKET NUMBER: 137-1061
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 354-3592
TELEFAX: (415) 857-1125
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 1261 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein

US-08-764-100-26

; APPLICANT: Duhl, David

; APPLICANT: Gorman, Susan W.

; APPLICANT: Leeng, Song

; APPLICANT: Sheffield, Val

; APPLICANT: Welch, Juliet

; TITLE OF INVENTION: CHANNEL-15 (CNCG-15) POLYNUCLEOTIDES, POLYPEPTIDES,

; FILE REFERENCE: 200130442

; CURRENT APPLICATION NUMBER: US/09/172,422A

; CURRENT FILING DATE: 1998-10-14

; NUMBER OF SEQ ID NOS: 3

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO: 1

; LENGTH: 2548

; TYPE: PRT

; ORGANISM: Homo sapien

; US-09-172-422-1

RESULT 2

US-08-687-399-7

; Sequence 7, Application US/08687399

; Patent No. 5928381

; GENERAL INFORMATION:

; APPLICANT: Toft, Annette H.

; ATTORNEY/AGENT INFORMATION:

; APPLICANT: Marchet, Dorthe

; ATTORNEY/AGENT INFORMATION:

; APPLICANT: Pedersen, Hanne H.

; ATTORNEY/AGENT INFORMATION:

; APPLICANT: Nilsson, Thomas E.

; ATTORNEY/AGENT INFORMATION:

; TITLE OF INVENTION: A Combined Desizing and Bleaching

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: No. 59283810 No. 5928381disk of No. 5928381th America, Inc.

; STREET: 405 Lexington Avenue, 64th Floor

; CITY: New York

; STATE: New York

; COUNTRY: United States of America

; ZIP: 10174-6401

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/687, 399

; FILING DATE:

; CLASSIFICATION: 008

; ATTORNEY/AGENT INFORMATION:

; NAME: Lambiris, Elias J.

; REFERENCE/DOCKET NUMBER: 33,728

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-878-9655

; TELEFAX: 212-867-0123

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1385 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; US-08-687-399-7

RESULT 3

US 09-172-422-1

; Sequence 1, Application US/09172422A

; Patent No. 6300485

; GENERAL INFORMATION:

; APPLICANT: Adams, Arwen E.

; ATTORNEY/AGENT INFORMATION:

; APPLICANT: Chin, Choi Ying

RESULT 4

US-08-462-467B-2

; Sequence 2, Application US/08462467B

; Patent No. 6210999

; GENERAL INFORMATION:

; APPLICANT: Rosenbaum, Jan S

; ATTORNEY/AGENT INFORMATION:

; APPLICANT: The Procter & Gamble Company

; STREET: 1810 East Miami River Road

; CITY: Ross

; STATE: OH

; COUNTRY: USA

; ZIP: 45061

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/462,467B

; FILING DATE:

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Hirscho, Bart S.

; REGISTRATION NUMBER: 32,572

; REFERENCE/DOCKET NUMBER: 5474R

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (513) 627-0633

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2887 amino acids

; TYPE: amino acid

; STRANDEDNESS: not relevant

; TOPOLOGY: protein

; MOLECULE TYPE: protein

RESULT 5

US-08-462-467B-2

Query Match 100.0%; Score 29; DB 4; Length 2887;
 Best Local Similarity 100.0%; Pred. No. 4.8e+02; Mismatches 0;
 Matches 6; Conservative 0; Indels 0; Gaps 0;

QY 1 LEPRAS 6
 Db 2034 LEPRAS 2039

RESULT 5
 US-08-462-467B-8
 Sequence 8, Application US/08462467B
 Patient No. 6210899

GENERAL INFORMATION:
 APPLICANT: Rosenbaum, Jan S
 TITLE OF INVENTION: The Use of a BMP Protein Receptor
 TITLE OF INVENTION: Complex for Screening Bone Metabolism Actives and Cells
 TITLE OF INVENTION: Co-Transfected With a Type II BMP Receptor and a Type I
 TITLE OF INVENTION: BMP Receptor
 NUMBER OF SEQUENCES: 39

CORRESPONDENCE ADDRESS:
 ADDRESSEE: The Procter & Gamble Company
 STREET: 11810 East Miami River Road
 CITY: Ross
 STATE: OH
 COUNTRY: USA
 ZIP: 45061

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US 08/032,235
 FILING DATE: 06-DEC-1996
 CLASSIFICATION: 800

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/214,064
 FILING DATE: 19-MAR-1996

ATTORNEY/AGENT INFORMATION:
 NAME: No. 5773700is Allen E.
 REGISTRATION NUMBER: 34,490
 REFERENCE/DOCKET NUMBER: 137-1061

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 354-3592
 TELEFAX: (415) 857-1225

INFORMATION FOR SEQ ID NO: 27:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3218 amino acids

TYPE: amino acid
 STRANDEDNESS: unknown
 TOPOLOGY: unknown
 MOLECULE TYPE: protein

INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2887 amino acids

TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: not relevant
 MOLECULE TYPE: protein

US-08-462-467B-8

RESULT 6
 US-08-764-100-27
 Sequence 8, Application US/08764100
 Patient No. 5773700

GENERAL INFORMATION:
 APPLICANT: van Gilsven J., Martinus Q.
 APPLICANT: De Haan, Petrus T.
 APPLICANT: Gielen L., Johannes J.
 APPLICANT: Peters, Dirk
 APPLICANT: Goldbach, Robert W.

TITLE OF INVENTION: Improvements in or Relating to Organic

Query Match 100.0%; Score 29; DB 4; Length 2887;
 Best Local Similarity 100.0%; Pred. No. 4.8e+02; Mismatches 0;
 Matches 6; Conservative 0; Indels 0; Gaps 0;

QY 1 LEPRAS 6
 Db 312 LEPRAS 317

RESULT 7
 US-08-652-816A-43
 Sequence 43, Application US/08652816A
 Patient No. 5872215

GENERAL INFORMATION:
 APPLICANT: Osbourn, JK
 APPLICANT: Allen, DJ
 APPLICANT: McCafferty, JG
 TITLE OF INVENTION: Specific binding members, materials and
 TITLE OF INVENTION: methods.
 NUMBER OF SEQUENCES: 53

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 STREET: 6300 Sears Tower, 233 South Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: United States of America

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, version #1.25 (EPO)

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/652,816A
 FILING DATE: 23-MAY-1996
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: GB 9125579.4
 FILING DATE: 02-DEC-1991
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: GB 9125579.8
 FILING DATE: 02-DEC-1991
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: GB 9206318.9
 FILING DATE: 24-MAR-1992
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: GB 9206372.6
 FILING DATE: 23-SEP-1992
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: GB 9206318.9
 FILING DATE: 07-DEC-1995
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: GB 9610824.6
 FILING DATE: 23-MAY-1996
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: PCW/GB92/02240
 FILING DATE: 02-DEC-1992
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/244,597
 FILING DATE: 01-JUN-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: David W. Clough
 REGISTRATION NUMBER: 36,107
 REFERENCE/DOCKET NUMBER: 26811/33308
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-474-6300
 INFORMATION FOR SEQ ID NO: 43:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 43 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FRAGMENT TYPE: internal
 US-08-652-816A-43

RESULT 8
 US-08-962-284-2
 ; Sequence 2, Application US/08962284
 ; General Information:
 ; Patent No. 5985608
 ; Best Local Similarity 83.3%; Score 26; DB 2; Length 43;
 ; Mismatches 5; Conservative 1; Indels 0; Gaps 0;
 ; Matches 1; Sequence 5, Application US/09335409
 ; Current Filing Date: 1999-06-17
 ; SEQ ID NO: 5
 ; LENGTH: 7257
 ; TYPE: PRT
 ; ORGANISM: Sorangium cellulosum
 ; US-09-335409-5

Query Match 89.7%; Score 26; DB 2; Length 1788;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03; Indels 0; Gaps 0;
 Matches 5; Conservative 1; Mismatches 0; Sequence 5, Application US/09335409
 ; Current Filing Date: 1999-06-17
 ; SEQ ID NO: 5
 ; LENGTH: 1788
 ; TYPE: PRT
 ; ORGANISM: Sorangium cellulosum
 ; US-09-335409-5

RESULT 9
 US-09-335409-5
 ; General Information:
 ; Patent No. 6121029
 ; Sequence 5, Application US/09335409
 ; Current Filing Date: 1999-06-17
 ; SEQ ID NO: 5
 ; LENGTH: 1788
 ; TYPE: PRT
 ; ORGANISM: Sorangium cellulosum
 ; US-09-335409-5

Query Match 89.7%; Score 26; DB 3; Length 7257;
 Best Local Similarity 83.3%; Pred. No. 5.4e+03; Indels 0; Gaps 0;
 Matches 5; Conservative 1; Mismatches 0; Sequence 5, Application US/09335409
 ; Current Filing Date: 1999-06-17
 ; SEQ ID NO: 5
 ; LENGTH: 7257
 ; TYPE: PRT
 ; ORGANISM: Sorangium cellulosum
 ; US-09-335409-5

OPERATING SYSTEM: Windows95
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/962,284
 FILING DATE: 31-OCT-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Fasse, Peter J. 32,983
 REGISTRATION NUMBER: 32,983
 REFERENCE/DOCKET NUMBER: 07917/058001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617/542-5070
 TELEFAX: 617/542-8906
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1788 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FRAGMENT TYPE: internal
 US-08-962-284-2

OPERATING SYSTEM: Windows95
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/962,284
 FILING DATE: 31-OCT-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Molnar, Istvan
 REGISTRATION NUMBER: 32,983
 REFERENCE/DOCKET NUMBER: 07917/058001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617/542-5070
 TELEFAX: 617/542-8906
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1788 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FRAGMENT TYPE: internal
 US-08-962-284-2

```

; APPLICANT: Zirkle, Ross
; APPLICANT: Cyr, Devon
; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
; FILE REFERENCE: 4-30582A
; CURRENT APPLICATION NUMBER: US/09/568,480
; CURRENT FILING DATE: 2000-05-10
; PRIORITY APPLICATION NUMBER: 09/335,409
; CURRENT FILING DATE: 2000-05-10
; PRIORITY FILING DATE: 1999-06-17
; PRIORITY FILING DATE: 1999-06-17
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 7257
; TYPE: PRT
; ORGANISM: Sorangium cellulosum
; US-09-568-102-5

Query Match          89.7%;  Score 26;  DB 4;  Length 7257;
Best Local Similarity 83.3%;  Pred. No. 5.4e+03;  Mismatches 1;  Indels 0;  Gaps 0;
Matches 5;  Conservative 1;  Mismatches 0;  Indels 0;  Gaps 0;

Qy    1 LEPRAS 6
      |||||
Db    2587 LDPNAS 2592

RESULT 11
US-09-567-969-5
; Sequence 5, Application US/09567969
; Patent No. 6355457
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Ligon, James
; APPLICANT: Molnar, Istvan
; APPLICANT: Zirkle, Ross
; APPLICANT: Cyr, Devon
; APPLICANT: Goerlach, Joern
; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
; FILE REFERENCE: 4-30582A
; CURRENT APPLICATION NUMBER: US/09/567, 969
; CURRENT FILING DATE: 2000-05-10
; PRIORITY FILING DATE: 1999-06-17
; PRIORITY FILING DATE: 1999-06-17
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 7257
; TYPE: PRT
; ORGANISM: Sorangium cellulosum
; US-09-567-969-5

Query Match          89.7%;  Score 26;  DB 4;  Length 7257;
Best Local Similarity 83.3%;  Pred. No. 5.4e+03;  Mismatches 1;  Indels 0;  Gaps 0;
Matches 5;  Conservative 1;  Mismatches 0;  Indels 0;  Gaps 0;

Qy    1 LEPRAS 6
      |||||
Db    2587 LDPNAS 2592

RESULT 13
US-09-568-486-5
; Sequence 5, Application US/09568486
; Patent No. 6355459
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Ligon, James
; APPLICANT: Molnar, Istvan
; APPLICANT: Zirkle, Ross
; APPLICANT: Cyr, Devon
; APPLICANT: Goerlach, Joern
; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
; FILE REFERENCE: 4-30582A
; CURRENT APPLICATION NUMBER: US/09/568, 486
; CURRENT FILING DATE: 2000-05-10
; PRIORITY FILING DATE: 1999-06-17
; PRIORITY FILING DATE: 1999-06-17
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 7257
; TYPE: PRT
; ORGANISM: Sorangium cellulosum
; US-09-568-486-5

Query Match          89.7%;  Score 26;  DB 4;  Length 7257;
Best Local Similarity 83.3%;  Pred. No. 5.4e+03;  Mismatches 1;  Indels 0;  Gaps 0;
Matches 5;  Conservative 1;  Mismatches 0;  Indels 0;  Gaps 0;

Qy    1 LEPRAS 6
      |||||
Db    2587 LDPNAS 2592

RESULT 14
US-09-568-472-5
; Sequence 5, Application US/09568472
; Patent No. 6358119
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Ligon, James
; APPLICANT: Molnar, Istvan
; APPLICANT: Zirkle, Ross
; APPLICANT: Cyr, Devon
; APPLICANT: Goerlach, Joern
; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
; FILE REFERENCE: 4-30582A
; CURRENT APPLICATION NUMBER: US/09/568, 472
; CURRENT FILING DATE: 2000-05-10
; PRIORITY FILING DATE: 1999-06-17
; PRIORITY FILING DATE: 1999-06-17
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 7257
; TYPE: PRT
; ORGANISM: Sorangium cellulosum
; US-09-568-472-5

```

CURRENT FILING DATE: 2000-05-10
 ; PRIOR APPLICATION NUMBER: 09/335,409
 ; PRIOR FILING DATE: 1999-06-17
 ; NUMBER OF SEQ ID NOS: 30
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 5
 ; LENGTH: 7357
 ; TYPE: PRT
 ; ORGANISM: *Sorangium cellulosum*
 ; US-09-568-472-5

Search completed: June 6, 2002, 13:04:11
 Job time: 23 sec

Query Match 89.7%; Score 26; DB 4; Length 7257;
 Best Local Similarity 83.3%; Pred. No. 5.4e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LEPPAS 6
 Db 2587 LDPRAS 2592

RESULT 15

US-08-808-982-8

; Sequence 8, Application US/08808982

PATENT NO. 5939271

GENERAL INFORMATION:

APPLICANT: Tessier-Lavigne, Marc

APPLICANT: Leonardo, E. David

APPLICANT: Hink, Lindsay

APPLICANT: Masu, Masayuki

APPLICANT: Kazuko, Keino-Masu

TITLE OF INVENTION: Netrin Receptors

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP

ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

STREET: 268 BUSH STREET, SUITE 3200

CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/808, 982

FILING DATE:

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: OSMAN, RICHARD A

REGISTRATION NUMBER: 36,627

REFERENCE/DOCKET NUMBER: UCG96-217

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 343-4341

TELEFAX: (415) 343-4342

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 102 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: not relevant

MOLECULE TYPE: peptide

US-08-808-982-8

Query Match 86.2%; Score 25; DB 2; Length 102;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEPPA 5
 Db 13 LEPPA 17

Thu Jun 6 15:17:14 2002

us-09-627-383-1.rai

THIS PAGE BLANK (USPTO)

as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000
 A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohn, J.D.; Junqueira, M.L.; Kemp, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramai, E.E.; Laing, chado, M.A.; Madeira, A.M.B.N.; Madeira, M.H.F.; Marino, C.L.; Marques, M.V.; Martins, E.A.; Authors: Martins, E.M.F.; Matsuoka, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; Rodrigues, V.; Rosa, A.J.; de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Savasak, A; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira, M.; Tsuhako, M.H.; Valada, H.; Van Sluys, M.A.; Verjovovski-Almeida, S.; Vettore, A.L.; Z A; Reference number: A59328
 A; Contents: annotation
 C; Genetics:
 A; Gene: XFI737

Query Match Similarity 100.0%; Score 29; DB 2; Length 242;
 Best Local Similarity 100.0%; Pred. No. 21; Mismatches 0; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LEPRAS 6
 Db 75 LEPRAS 80

RESULT 3

T46354

hypothetical protein DKFZp434F1016.1 - human (fragment)

C;Species: Homo sapiens (man)
 C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 02-Sep-2000C;Accession: T46354
 C;Author: K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
 C;Submitted to the Protein Sequence Database, January 2000
 A;Reference number: 223037A;Accession: T46354
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-1397 <AAA>A;Cross-references: EMBL:AL137287
 A;Experimental source: adult testis; clone DKFZp434F1016C;Genetics:
 C;Note: DKFZp434F1016.1
 C;Superfamily: protein kinase C zinc-binding repeat homology
 C;Domain: protein kinase C zinc-binding repeat homology <KZN>Query Match Similarity 100.0%; Score 29; DB 2; Length 1397;
 Best Local Similarity 100.0%; Pred. No. 1.4e-02; Mismatches 0; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LEPRAS 6
 Db 1206 LEPRAS 1211

RESULT 4

T31099

myosin-RhGAP protein, Myr 7 - rat

C;Species: Rattus norvegicus (Norway rat)
 C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 08-Sep-2000C;Accession: T31099
 C;Author: Chieregatti, E.; Gaertner, A.; Stoefler, H.E.; Baehler, M.
 C;Submitted to the EMBL Data Library, October 1997
 A;Reference number: 220982A;Accession: T31099
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-2626 <CH1>
 A;Cross-references: EMBL:AJ001713; NID:e1357083; PID:e1357084; PLDN:CAA04946.1
 A;Experimental source: strain Sprague-Dawley
 C;Genetics:
 A;Gene: myoga

Query Match Similarity 100.0%; Score 29; DB 2; Length 2626;
 Best Local Similarity 100.0%; Pred. No. 2.7e-02; Mismatches 0; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LEPRAS 6
 Db 2443 LEPRAS 2448

RESULT 5

JC5476

junction-specific DNA-binding protein ruvA - Pseudomonas aeruginosa

N;Alternate names: Holliday junction DNA helicase RuVA

C;Species: Pseudomonas aeruginosa

C;Date: 07-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 31-Dec-2000

C;Accession: JC5476; H8324

R;Hishida, T.; Iwasa, K.; Ishioka, K.; Shinagawa, H.

A;Title: Molecular analysis of the Pseudomonas aeruginosa genes, ruvA, ruvB and ruvC,

A;Reference number: JC5476; MOID:97136691

A;Accession: JC5476

A;Molecule type: DNA

A;Residues: 1-201 <KIS>

A;Cross-references: DDBJ:D83138; NID:91183837; PID:BA11818.1; PID:91183841

A;Experimental source: strain PA01

A;Note: the authors translated the initiation codon GNG for residue 1 as Met

R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Kish, M.J.;

Adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L

; Lory, S.; Olson, M.V.

R;Nature 406, 959-964, 2000

A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa

A;Reference number: A82950; MOID:20437337

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-201 <STO>

A;Cross-references: GB:AB004530; GB:AE004091; NID:99946865; PID:AAQ04355.1; GSPDB:GN

F;849-897/Domain: protein kinase C zinc-binding repeat homology <KZN>

C;Superfamily: protein kinase C zinc-binding repeat homology <KZN>

C;Domain: protein kinase C zinc-binding repeat homology <KZN>

C;Genetics:
 C;Function:

A;Gene: ruvA; PA0965

A;Start codon: GTG

A;Description: acting as specificity factor that targets ruvB protein; ruvA protein a

C;Superfamily: homologous genetic recombination and DNA repair

C;Keywords: DNA binding; DNA recombination; DNA repair

Query Match Similarity 93.1%; Score 27; DB 2; Length 201;
 Best Local Similarity 83.3%; Pred. No. 53; Mismatches 0; Indels 0; Gaps 0;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LEPRAS 6
 Db 146 MEPRAS 151

Query Match Similarity 100.0%; Score 29; DB 2; Length 2626;
 Best Local Similarity 100.0%; Pred. No. 2.7e-02; Mismatches 0; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LEPRAS 6
 Db 2443 LEPRAS 2448

RESULT 6

G95376

conserved hypothetical protein SMA1676 [imported] - Sinorhizobium meliloti (strain 10

C;Species: Sinorhizobium meliloti

C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001

C;Accession: G95376

R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barlow-Hubler, F.; B

; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.G.; Surzycki, R.; Wells, D.H.; Yeh, K

; Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001

A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meli

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 04-Mar-2000
 C;Accession: T38882
 R;Murphy, L.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
 submitted to the EMBL Data Library, February 1996
 A;Reference number: 221807
 A;Accession: T38882
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: DNA
 A;Residues: 1-391 <MUR>
 A;Cross-references: EMBL:Z69380; PIDN:CAA93341.1; GSPDB:GN00066; SPDB:SPAC4H3.02C
 A;Experimental source: strain 972h-; cosmid c4H3
 C;Genetics:
 A;Gene: SPDB:SPAC4H3.02C
 A;Map position: 1
 A;Map: 56/2
 C;Superfamily: Schizosaccharomyces pombe hypothetical protein SPAC4H3.02C

Query Match 89.7% Score 26; DB 2; Length 391;
 Best Local Similarity 83.3%; Pred. No. 1.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 LEPRAS 6
 Db 37 LQPRAS 42

RESULT 15
 A;H0373
 Cysteine--tRNA ligase (EC 6.1.1.16) [imported] - Yersinia pestis (strain CO92)
 C;Species: Yersinia pestis
 C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001
 C;Accession: A;H0373
 R;Parthill, J.; Wien, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
 deno-Tarrada, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
 ill, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, J.;
 Nature 413, 523-527, 2001
 A;Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.
 A;Reference number: AB0001; MUID:21470413; PMID:11586360
 A;Accession: A;H0373
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-461 <KIR>
 A;Cross-references: GB:AL590842; PIDN:CAC92315.1; PID:gi15981026; GSPDB:GN00175
 C;Genetics:
 A;Gene: cysS
 C;Superfamily: cysteine--tRNA ligase
 C;Keywords: ligase

Query Match 89.7% Score 26; DB 2; Length 461;
 Best Local Similarity 83.3%; Pred. No. 2.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 LEPRAS 6
 Db 110 LEPRAT 115

Search completed: June 6, 2002, 13:04:33
 Job time: 45 sec

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using SW model.

Run on: June 6, 2002, 13:04:38 ; Search time 10.31 Seconds

Minimum DB seq length: 0 (without alignments)
Maximum DB seq length: 200000000
22.533 Million cell updates/sec

Title: US-09-627-383-1
Perfect score: 29
Sequence: 1 LEPRAS 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : SwissProt_40;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	29	100.0	1026	1	TAC2_HUMAN	095359 homo sapien
2	27	93.1	201	1	RUVA_PSEAE	051425 pseudomonas
3	26	89.7	238	1	RMO8_YEAST	P22353 saccharomyces
4	26	89.7	335	1	B3G3_CRIGR	09w447 cricketulus
5	26	89.7	335	1	B3G3_HUMAN	094166 homo sapien
6	26	89.7	335	1	B3G3_MOUSE	P58158 mus musculus
7	26	89.7	391	1	AY22_SCHPO	Q10201 schizosaccharomyces
8	26	89.7	465	1	SYC_HELP	Q9z2w6 helicobacte
9	26	89.7	465	1	TAIT_SCHPO	P41259 helicobacte
10	26	89.7	561	1	ALUL_HUMAN	Q08984 schizosaccharomyces
11	26	89.7	591	1	TPN9_ECOLI	P39188 homo sapien
12	26	89.7	710	1	PKN6_MYXAA	P51738 myxococcus
13	26	89.7	821	1	CANJ_RAT	P16259 rattus norvegicus
14	26	89.7	836	1	RPOC_CHLVO	P50300 chlorella vulgaris
15	26	89.7	978	1	PEX6_RAT	P57777 rattus norvegicus
16	26	89.7	986	1	DPO1_NFVBM	P41712 bombyx mori
17	26	89.7	988	1	TNP9_ECOLI	P51565 escherichia
18	26	89.7	2194	1	SC16_YEAST	P48415 saccharomyces
19	26	89.7	4753	1	LRP_CAEEL	Q04833 caenorhabditis
20	25	86.2	190	1	DSRG_HUMAN	P57055 caenorhabditis
21	25	86.2	287	1	UL24_ITLVT	P23986 infectious
22	25	86.2	295	1	ACTR_SHEEP	Q9t777 ovis aries
23	25	86.2	297	1	ACTR_BOVIN	P34974 bos taurus
24	25	86.2	300	1	MOVF_AMYVA	P03595 alfalfa mos
25	25	86.2	300	1	MOVF_ANMVA	P05672 alfalfa mos
26	25	86.2	300	1	MOVF_AMVFA	P03596 alfalfa mos
27	25	86.2	300	1	MOVF_AMVGS	P24265 alfalfa mos
28	25	86.2	309	1	NUSG_STRG8	P37852 streptomyces
29	25	86.2	430	1	SGK_RAT	Q06226 rattus norvegicus
30	25	86.2	431	1	SGK_HUMAN	Q00141 homo sapien
31	25	86.2	431	1	SGK_MOUSE	Q9wrc6 mus musculus
32	25	86.2	431	1	SGK_RABIT	Q9x18 oryctolagus
33	25	86.2	452	1	F26 YEAST	P32604 saccharomyces

DR	EMBL: AAF220152; AAF29537.2; -.	CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
KW	Coiled coil; Nuclear protein; Alternative splicing.	CC	-----
FT	43 51	DR	-----
DOMAIN	498 501	EMBL	D83138; BRA11818.1; -.
FT	753 781	DR	-----
DOMAIN	824 1025	EMBL	AE004530; AAG04355.1; -.
FT	507 510	DR	HSSP; P08576; ICKU.
FT	711 787	DR	-----
FT	44 67	DR	InterPro; IPR003583; HHH.1.
CONFLICT		DR	InterPro; IPR000085; RuVA.
FT		DR	Pfam; PF01330; RuVA; 1.
FT		DR	Pfam; PF02904; RuVA; 1.
FT		DR	ProDom; P0006248; RuVA; 1.
SQ	SEQUENCE 1026 AA; 112110 MW; E2575FCB4689CFB CRC64;	DR	SMART; SM00278; HH1.2.
Query Match	100.0%; Score 29; DB 1; Length 1026;	KW	DNA repair; SOS response; ATP-binding; DNA recombination; Helicase;
Best Local Similarity	100.0%; Pred. No. 49;	CC	-----
Matches	6; Conservative 0; Mismatches 0;	CC	-----
QY	1 LEPRAS 6	CC	-----
Db	130 LEPRAS 135	CC	-----
RESULT 2		CC	-----
RUVA_PSEAE		CC	-----
ID		CC	-----
AC	051425;	STANDARD;	PRT; 201 AA.
DT	01-NOV-1997 (Rel. 35, Created)	CC	-----
DT	01-NOV-1997 (Rel. 35, Last sequence update)	CC	-----
DT	16-OCT-2001 (Rel. 40, Last annotation update)	CC	-----
DE	Holiday junction DNA helicase RuVA.	CC	-----
GN	GN PA0966.	CC	-----
OS	Pseudomonas aeruginosa.	CC	-----
OC	Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;	CC	-----
OC	Pseudomonads.	CC	-----
OX	NCBI_TAXID=287;	CC	-----
RN	[1]	CC	-----
RP	SEQUENCE FROM N.A.	CC	-----
RC	STRAIN=ATCC 15692 / PA01;	CC	-----
RX	MEDLINE=97136691; PubMed=8982068;	CC	-----
RA	Hishida T., Iwasaki H., Ishioka K., Shinagawa H.	CC	-----
RT	"Molecular analysis of the Pseudomonas aeruginosa genes, ruva, ruvb and ruvc involved in processing of homologous recombination intermediates."	CC	-----
RT	Gene 182:63-70(1996).	CC	-----
RL	[2]	CC	-----
RP	SEQUENCE FROM N.A.	CC	-----
RC	STRAIN=ATCC 15692 / PA01;	CC	-----
RX	MEDLINE=0437337; PubMed=1098043;	CC	-----
RA	Stover C.K., Pham X.-Q.T., Elwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Huffnagle W.O., Kowalik D.J., Lagrou M., Gardner R.L., Goletz L., Tolentino E., Westbroek-Wadman S., Yuan Y., Brody L.J., Coulter S.N., Folger K.R., Kas A., Larbig K., Jim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Salter M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen.";	CC	-----
RT	Nature 406:959-964(2000).	CC	-----
RL	-----	CC	-----
CC	-!- FUNCTION: THE RUVA RUVB COMPLEX IN THE PRESENCE OF ATP RENATURES CRUICIFORM STRUCTURE IN SUPERCOILED DNA WITH PALINDROMIC SEQUENCE, INDICATING THAT IT MAY PROMOTE STRAND EXCHANGE REACTIONS IN HOMOLOGOUS RECOMBINATION. RUVAB IS AN HELICASE THAT MEDIATES THE HOLIDAY JUNCTION MIGRATION BY LOCALIZED DENATURATION AND REANNELING. RUVA STIMULATES, IN THE PRESENCE OF DNA, THE WEAK ATPase ACTIVITY OF RUVB (BY SIMILARITY).	CC	-----
CC	-!- SUBUNIT: FORMS A COMPLEX WITH RUVB.	CC	-----
CC	-!- SIMILARITY: BELONGS TO THE L17P FAMILY OF RIBOSOMAL PROTEINS.	CC	-----
CC	-!- SUBCELLULAR LOCATION: Mitochondrial.	CC	-----
CC	-!- SIMILARITY: BELONGS TO THE L17P FAMILY OF RIBOSOMAL PROTEINS.	CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	CC	-----
DR	EMBL: X53841; CAA37834.1; -.	CC	-----
DR	EMBL: Z34288; CAA80060.1; -.	CC	-----
DR	EMBL: Z49338; CAA89354.1; -.	CC	-----
DR	PIR: S14890; S14890.	CC	-----
DR	PIR: S47128; S47128.	CC	-----
SGD	S0003599; MRPL8.	CC	-----

DR	InterPro; IPR00456; Ribosomal_L17.
DR	pfam; PF01196; Ribosomal_L17; 1.
DR	PRODOM; PD004277; Ribosomal_L17; 1.
KW	Ribosomal protein; Mitochondrion.
FT	CONFLICT 82. D -> G (IN REF. 1).
SQ	SEQUENCE 238 AA; 26945 MW; A130EFD95E8719BA CRC64;
QY	1 LEPRAS 6
Db	111 LEPRAN 116
RESULT 4	Query Match 89.7%; Score 26; DB 1; Length 238; Best Local Similarity 83.3%; Pred. No. 51; Mismatches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
ID B3G3_CRIGR	STANDARD; PRT; 335 AA.
AC Q9WU47	DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)	DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Galactosylgalactosylxylosylprotein 3-beta-glucuronosyltransferase 3	DE (EC 2.4.1.135) (Beta-1,3-glucuronosyltransferase-1) (GICAT-1) (UDP-GICUA:Gal Beta-1,3-Gal-R glucuronosyltransferase) (GICAT-1).
DE B3GAT3	GN Cricetulus griseus (Chinese hamster).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae; Cricetus	OC NCBI_TAXID=10029; RN [1] SEQUENCE FROM N.A. MEDLINE=99175158; PubMed=10075568;
RX	RA Wei G., Bai X., Sarkar A.K., Esko J.D.; "Formation of HNK-1 determinants and the glycosaminoglycan tetrasaccharide linkage region by UDP-GICUA:Galactose beta-1,3-glucuronosyltransferases."
RT	J. Biol. Chem. 274:7857-7864 (1999).
RT	J- FUNCTION: GLYCOSAMINOGLYCANS BIOSYNTHESIS. INVOLVED IN FORMING THE LINKAGE TETRASACCHARIDE PRESENT IN HEPARAN SULFATE AND CHONDROITIN SULFATE. TRANSFERS A GLUCURONIC ACID MOIETY FROM THE URIDINE DIPHOSPHATE-GLUCURONIC ACID (UDP-GICUA) TO THE COMMON LINKAGE REGION TRISACCHARIDE GAL BETA 1-3GAL BETA 1-4Xyl COVALENTLY BOUND TO A SER RESIDUE AT THE GLYCOSAMINOGLYCAN ATTACHMENT SITE OF PROTEOGLYCANS. CAN ALSO PLAY A ROLE IN THE BIOSYNTHESIS OF L2/HNK-1 CARBOHYDRATE EPITOPE ON GLYCOPROTEINS. HIGHEST ACTIVITY SEEN WITH GAL-BETA-1, 3-GAL-BETA-O-R (WHERE R=NAFTALENEMETHANOL OR BENZYL ALCOHOL).
CC	-!- CATALYTIC ACTIVITY: UDP-glucuronate + 3-beta-D-galactosyl-4-beta-D-galactosyl-O-beta-D-xylosylprotein = UDP + 3-beta-D-xylosylprotein.
CC	-!- COFACTOR: MANGANESE.
CC	-!- PATHWAY: GLYCOSYLATION.
CC	-!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC	-!- SUBCELLULAR LOCATION: TYPE II membrane protein. Golgi.
CC	-!- TISSUE SPECIFICITY: LIVER, BRAIN AND HEART. MODERATE EXPRESSION SEEN IN LUNG, SKELETAL MUSCLE, KIDNEY AND TESTIS.
CC	-!- PTM: N-GLYCOSYLATED (BY SIMILARITY).
CC	-!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 43.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC	-----
CC	DR EMBL; AF113703; BAA22007.1; -.
DR	DR HSSP; 094765; 1FGG.
DR	PROSITE; PS01167; RIBOSOMAL_L17; 1.
KW	Manganese; Multigene family.
FT	DOMAIN 1 7 CYTOPLASMIC (POTENTIAL), SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT	TRANSMEM 8 28 (POTENTIAL), LUMINAL, CATALYTIC (POTENTIAL).
FT	DOMAIN 2 9 335 CATALYTIC BASE (BY SIMILARITY).
FT	ACT_SITE 281 281 MANGANESE (BY SIMILARITY).
FT	METAL 196 196 INTRACHAIN (BY SIMILARITY).
FT	DISULFID 33 33 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD 300 300 B4FDD1645BDCCDIC CRC64;
SQ	SEQUENCE 335 AA; 37095 MW; B4FDD1645BDCCDIC CRC64;
QY	1 LEPRAS 6
Db	294 LEPRAA 299
RESULT 5	Query Match 89.7%; Score 26; DB 1; Length 335; Best Local Similarity 83.3%; Pred. No. 74; Mismatches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
ID B3G3_HUMAN	STANDARD; PRT; 335 AA.
AC O94766; Q9UBP0; DT 16-OCT-2001 (Rel. 40, Created)	DT 01-MAR-2002 (Rel. 41, Last sequence update)
DE B3GAT3	DE Galactosylgalactosylxylosylprotein 3-beta-glucuronosyltransferase 3 (EC 2.4.1.135) (Beta-1,3-glucuronosyltransferase 3) (GICAT-1) (UDP-GICUA:Gal beta-1,3-Gal-R glucuronosyltransferase) (GICAT-1).
DE	GN BIGAT3.
DE	OS Homo sapiens (Human).
OC	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarhini; Homidae; Homo.
OX NEBI_TAXID=9606;	RN [1] SEQUENCE FROM N.A. AND CHARACTERIZATION.
RP	RC TISSUE=Placenta;
RP	RX MEDLINE=98175919; PubMed=9506957;
RA	RX Kitagawa H., Tone Y., Tamura J.-I., Neumann K.W., Ogawa T., Oka S., Kawasaki T., Sugahara K.; "Molecular cloning and expression of glucuronosyltransferase I involved in the biosynthesis of the glycosaminoglycan-protein linkage region of proteoglycans." J. Biol. Chem. 273:6615-6618 (1998).
RT	RX [2] SEQUENCE FROM N.A., CHARACTERIZATION, AND MUTAGENESIS.
RP	RX MEDLINE=2042846; PubMed=10842173;
RA	RX Ouzzine M., Gilberti S., Netter P., Magdalou J., Fournel-Gigleux S.; "Structure/function of the human Galbeta1,3-glucuronosyltransferase. Bineration and functional activity are mediated by two crucial cysteine residues"; J. Biol. Chem. 275:28254-28260 (2000).
RN	RN [3] SEQUENCE OF 9-335 FROM N.A.
RP	RC TISSUE=Brain;
RP	RX MEDLINE=99128347; PubMed=9922767;
RA	RX Herman T., Horvitz H.R.; "Three proteins involved in <i>Caenorhabditis elegans</i> vulval invagination are similar to components of a glycosylation pathway." Proc. Natl. Acad. Sci. U.S.A. 96:974-979 (1999).
RT	RX [4] CHARACTERIZATION.
RP	RX MEDLINE=99456856; PubMed=10526176;
RA	RX Tone Y., Kitagawa H., Imiya K., Oka S., Kawasaki T., Sugahara K.; "Characterization of recombinant human glucuronosyltransferase I involved in the biosynthesis of the glycosaminoglycan-protein linkage

RT region of proteoglycans";
 RL FEBs Lett. 459:415-420(1999).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF 76-335.
 RC TISSUE=Liver;
 RX MEDLINE=20057909; PubMed=10946001;
 RA Negishi M.;
 RA Pedersen L.C.; Tsuchida K.; Kitagawa H.; Sugahara K.; Darden T.A.;
 RA "Heparan/chondroitin sulfate biosynthesis. Structure and mechanism of
 human glucuronoyltransferase 1";
 RT J. Biol. Chem. 275:34580-34585 (2000).
 CC -I- FUNCTION: GLYCOSAMINOGLYCAN BIOSYNTHESIS. INVOLVED IN FORMING THE
 LINKAGE TERASACCHARIDE PRESENT IN HEPARAN SULFATE AND CHONDRITIN
 SULFATE. TRANSFERS A GLUCURONIC ACID MOIETY FROM THE URIDINE
 DIPHOSPHATE-GLUCURONIC ACID (UDP-GCUC) TO THE COMMON LINKAGE
 REGION TRISACCHARIDE GAL BETA 1->GAL BETA 1->XYL COVALENTLY BOUND
 TO A SER RESIDE AT THE GLYCOSAMINOGLYCAN ATTACHMENT SITE OF
 PROTOGLYCAN. CAN ALSO PLAY A ROLE IN THE BIOSYNTHESIS OF L2/HNK-
 1 CARBOHYDRATE EPITOPE ON GLYCOPROTEINS. SHOWS STRICT SPECIFICITY
 FOR GAL BETA1-3GAL BETA1-4XYL, EXHIBITING NEGLIGIBLE INCORPORATION
 INTO OTHER GALACTOSIDE SUBSTRATES INCLUDING GALBETA1-3GAL BETA1-O-
 BENZYL, GALBETA1-4GLUCNAc AND GALBETA1-4GIC.
 CC -I- CATALYTIC ACTIVITY: UDP-**l**-glucuronate + 3-beta-D-galactosyl-4-
 beta-D-galactosyl-O-beta-D-xylosylprotein = UDP + 3-beta-D-
 glucuronosyl-3-beta-D-galactosyl-4-beta-D-galactosyl-O-beta-D-
 xylosylprotein.
 CC -I- COFACTOR: MANGANESE.
 CC -I- ENZYME REGULATION: INHIBITED BY EDTA.
 CC -I- PATHWAY: GLYCOSYLATION.
 CC -I- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
 CC -I- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. Golgi
 -I- TISSUE SPECIFICITY: UBIQUITOUS (BUT WEAKLY EXPRESSED IN ALL TISSUES
 EXAMINED).
 CC -I- PTM: N-GLYCOSYLATED.
 CC -I- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 43.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC
 CC EMBL; AB0109598; BAA34537; 1; -.
 CC EMBL; AJ005865; CA06742; 1; -.
 CC MIM; 606374; -.
 CC PDB; 1FGG; 31-JAN-01.
 CC KW TRANSFERASE; GLYCOPROTEIN; TRANSMEMBRANE; SIGNAL-ANCHOR; Golgi stack;
 KW Manganese; Multigene family; 3D-structure.
 CC DOMAIN 1
 CC DOMAIN 7
 CC TRANSMEM 8
 CC 28
 CC SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 CC (POTENTIAL).
 CC DOMAIN 29
 CC 335
 CC DISULFID 33
 CC 33
 CC CARBOHYD 300
 CC 300
 CC ACT-SITE 281
 CC 281
 CC METAL 196
 CC 196
 CC MUTAGEN 33
 CC 33
 CC MUTAGEN 301
 CC 301
 CC CONFLICT 204
 CC 204
 CC SEQUENCE 335 AA;
 CC 37061 MW;
 CC 5ED4550428636C0F CRC64;
 CC
 CC Query Match 89.7%; Score 26; DB 1; Length 335;
 CC Best Local Similarity 83.3%; Pred. No. 74;
 CC Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC Qy 1 LEPRSS 6
 CC Db 294 LEPRSSA 299

RESULT 6
 ID B3G3_MOUSE
 ID B3G3_MOUSE
 ID STANDARD;
 ID PRT; 335 AA.
 AC P58138;
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Galactosylgalactosylxylosylprotein 3-beta-D-glucuronosyltransferase 3
 DE (EC 2.4.1.135) (Beta-1,3-glucuronosyltransferase 3)
 DE (Glucuronosyltransferase-I) (GICAT-1) (UDP-GlCUA:Gal Beta1,3-Gal-R
 DE Glucuronosyltransferase) (GlcUAT-1).
 DE GN B3GAT3;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxId=10090;
 RN [1]
 RP TISSUE=breast tumor;
 RA Strausberg R.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 CC -I- FUNCTION: GLYCOSAMINOGLYCAN BIOSYNTHESIS. INVOLVED IN FORMING THE
 LINKAGE TERASACCHARIDE PRESENT IN HEPARAN SULFATE AND CHONDRITIN
 SULFATE. TRANSFERS A GLUCURONIC ACID MOIETY FROM THE URIDINE
 DIPHOSPHATE-GLUCURONIC ACID (UDP-GCUC) TO THE COMMON LINKAGE
 REGION TRISACCHARIDE GAL BETA 1->GAL BETA 1->XYL COVALENTLY BOUND
 TO A SER RESIDE AT THE GLYCOSAMINOGLYCAN ATTACHMENT SITE OF L2/HNK-
 1 CARBOHYDRATE EPITOPE ON GLYCOPROTEINS (BY SIMILARITY).
 CC -I- CATALYTIC ACTIVITY: UDP-**l**-glucuronate + 3-beta-D-galactosyl-4-
 beta-D-galactosyl-O-beta-D-xylosylprotein = UDP + 3-beta-D-
 glucuronosyl-3-beta-D-galactosyl-4-beta-D-galactosyl-O-beta-D-
 xylosylprotein.
 CC -I- COFACTOR: MANGANESE (BY SIMILARITY).
 CC -I- PATHWAY: GLYCOSYLATION.
 CC -I- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
 CC -I- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 43.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC
 CC EMBL; BC002103; AAB01013; 1; -.
 CC KW TRANSFERASE; GLYCOPROTEIN; TRANSMEMBRANE; Signal-anchor; Golgi stack;
 KW Manganese; Multigene family.
 CC DOMAIN 1
 CC DOMAIN 7
 CC TRANSMEM 8
 CC 28
 CC SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 CC (POTENTIAL).
 CC DOMAIN 29
 CC 335
 CC ACT-SITE 281
 CC 281
 CC METAL 196
 CC 196
 CC DISULFID 33
 CC 33
 CC CARBOHYD 300
 CC 300
 CC ACT-SITE 281
 CC 281
 CC METAL 196
 CC 196
 CC MUTAGEN 33
 CC 33
 CC C->A: ENZYME INACTIVATION AND LOSS OF
 GLYCOSYLATION.
 CC S -> F (IN REF. 3).
 CC SEQUENCE 335 AA;
 CC 37067 MW;
 CC 906EED2AB672F1EC CRC64;
 CC
 CC Query Match 89.7%; Score 26; DB 1; Length 335;
 CC Best Local Similarity 83.3%; Pred. No. 74;
 CC Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC Qy 1 LEPRSS 6
 CC Db 294 LEPRSSA 299

RESULT 7
 VAY2-SCHPO STANDARD; PRT; 391 AA.
 ID YAY2-SCHPO
 AC 010210;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Hypothetical 44.7 kDa protein C4H3.02C in chromosome I.
 GN SPAC113.02C.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomyces; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae; NCBI_TaxID=4896;
 OX [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=972;
 RA Murphy L., Harris D., Barrell B.G., Rajandream M.A., Walsh S.V.;
 RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC
 CC
 DR EMBL; AE001511; AAD065999.1; -
 DR InterPro; IPR021208; tRNA synt_1e.
 DR InterPro; IPR01412; tRNA_synt_1.
 DR PR0106; tRNA-synt_1c; 1.
 DR PRINTS; PR00983; TRNAsYNTcys.
 DR PROSITE; PS00178; AA_TRNA_LIGASE_I; FALSE_NEG.
 DR Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding; KW Complete protein.
 FT SITE 29 39 "HIGH" REGION.
 FT BINDING 272 273 "KASKS" REGION.
 SQ SEQUENCE 465 AA; 53306 MW; 336AE8BAE0D4476A CRC64;
 KW Hypothetical protein.
 SQ SEQUENCE 391 AA; 44716 MW; 72D8F088B15E50A8 CRC64;

RESULT 8
 Query Match 89.7%; Score 26; DB 1; Length 391;
 Best Local Similarity 83.3%; Pred. No. 87;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 ID SYC_HELPJ STANDARD; PRT; 465 AA.
 AC 09ZKWC;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Cysteinyl-tRNA synthetase (EC 6.1.1.16) (Cysteine-tRNA ligase) (CYSRS).
 GN CYSS OR JHP0818.
 OS Helicobacter pylori J99 (Campylobacter pylori J99).
 OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
 OC Helicobacter.
 OX NCBI_TaxID=85963;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99120557; PubMed=9923582;
 RA Alm R.A., Ling L.-S.L., Moir B.T., King B.L., Brown E.D., Dolg P.C., Smith D.R., Noonan B., Guild B.L., Carmel G., Tummolo P.J., Caruso A., Urias-Nickelsen M., Mills D.M., Ives C., Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F., Trust T.J.;
 RA "Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori.";
 RA Smith D.R., Noonan B., Guild B.L., Carmel G., Tummolo P.J., Caruso A., Urias-Nickelsen M., Mills D.M., Ives C., Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F., Trust T.J.;
 RA "The complete genome sequence of the gastric pathogen Helicobacter pylori.";
 RA Nature 397:176-180 (1999).
 CC -1- CATALYTIC ACTIVITY: AMP + L-cysteine + tRNA(CYS) = AMP + diphosphate + L-cysteinyl-tRNA(CYS).
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Cyttoplasmic.
 CC -1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.

RESULT 9
 Query Match 89.7%; Score 26; DB 1; Length 465;
 Best Local Similarity 83.3%; Pred. No. 1.1e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 ID SYC_HELPY STANDARD; PRT; 465 AA.
 AC P41259;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Cysteinyl-tRNA synthetase (EC 6.1.1.16) (Cysteine-tRNA ligase) (CYSRS).
 GN CYSS OR HP0886.
 OS Helicobacter pylori (Campylobacter pylori).
 OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
 OC Helicobacter.
 OX NCBI_TaxID=210;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9739467; PubMed=9252185;
 RA Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G., Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty S., Nelson K., Quackenbush J.J., Zhou L., Kirkness E.F., Peterson S., Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A., McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K., Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M., Cotton M.D., Weigman J.M., Fujii C., Bowman C., Watthey L., Wallin E., Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M., Venter J.C.,
 RA "The complete genome sequence of the gastric pathogen Helicobacter pylori.";
 RA Nature 388:539-547 (1997).
 RN [2]
 RP SEQUENCE OF 278-465 FROM N.A.
 RX MEDLINE=94193753; PubMed=8144644;
 RA Cover T.L., Tummolo M.K., Cao P., Thompson S.A., Blaser M.J.;
 RT "Divergence of genetic sequences for the vacuolating cytotoxin among Helicobacter pylori strains";
 RT J. Biol. Chem. 269:10566-10573 (1994).
 RN [3]
 RP SEQUENCE OF 407-465 FROM N.A.

RA STRAIN=CCUG 17874 / NCCTC 11638;
 RX MEDLINE=9-222314; PubMed=8168917;
 RA Phanidis S.H., Ilver D.J., Janzon L., Normark S., Westblom T.U.;
 RT "Pathological significance and molecular characterization of the vacuolating toxin gene of *Helicobacter pylori*.";
 RL *Immunol. 62:1557-1565(1994)*
 CC -!- CATALYTIC ACTIVITY: ATP + L-Cysteine + tRNA(Cys) = AMP +
 CC diphosphate + L-Cysteinyl-tRNA(Cys).
 -!- SUBUNIT: MONOMER (BY SIMILARITY).
 -!- SUBCELLULAR LOCATION: Cytoplasmic.
 -!- SIMILARITY: BELONGS TO CLASS I AMINOCYCL-TRNA SYNTHETASE FAMILY.
 -!- STRONG, TO METHIONYL-TRNA SYNTHETASE.

CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non Profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC CC
 CC CC DR EMBL: A000598; AAC07934; 1; -.
 DR EMBL: U05677; AAC17656; 1; -.
 DR EMBL: U01145; AAA18866; 1; -.
 DR PIR: C53739; C53739.
 DR TIGR: H00866; DR InterPro: IPR02308; tRNA-synt_1e.
 DR InterPro: IPR01412; tRNA-synt_1.
 DR Pfam: PF01406; tRNA-synt_1e; 1.
 DR PRINTS: PR00933; tRNA-SYNTHCYS.
 DR PROSITE: PS00178; AA-TRNA-LIGASE_I; FALSE_NEG.
 KW Aminocycl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding; Complete proteome.
 FT SITE 29 "HIGH" REGION.
 FT SITE 269 273 "KMSKS" REGION.
 FT BINDING 272 277 ATP (BY SIMILARITY).
 FT VARIANT 280 280 V -> I (IN STRAIN ATCC 49503).
 FT VARIANT 332 332 T -> V (IN STRAIN ATCC 49503).
 FT VARIANT 392 392 N (IN STRAIN ATCC 49503).
 FT VARIANT 432 432 R -> Q (IN STRAINS ATCC 49503 AND NCCTC 11638).
 FT VARIANT 434 434 D -> N (IN STRAIN NCCTC 11638).
 FT VARIANT 440 440 S -> H (IN STRAIN ATCC 49503).
 SQ SEQUENCE 465 AA; 53131 MW; B7053D58BCD8/F30 CRC64;

RESULT 11 ALU1_HUMAN
 ID ALU1_HUMAN STANDARD; PRT; 591 AA.
 AC P39188;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Alu subfamily J sequence contamination warning entry.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TAXID=9606;
 RN [1] RPI_SEQUENCE FROM N.A.
 RX MEDLINE=95021758; PubMed=7935834;
 RA Claverie J.M., Makalowski W.;
 RT "Alu alert.";
 RL Nature 371:752-752(1994).
 RL [2]
 RP CONCEPT;
 RX MEDLINE=92241891; PubMed=1572661;
 RA Claverie J.M.;
 RT "Identifying coding exons by similarity search: alu-derived and other potentially misleading protein sequences.";
 RL [3] Genomics 12:838-841(1992).
 RN ALU FAMILIES CLASSIFICATION;
 RP MEDLINE=88333009; PubMed=313842;
 RA Quentin Y.;
 RT "The Alu family developed through successive waves of fixation closely connected with primate lineage history.";
 RL J. Mol. Evol. 27:194-202(1998).
 RN [4]
 RP ALU FAMILIES CLASSIFICATION.
 RX MEDLINE=91178815; PubMed=1706781;
 RA Jurka J., Milosavljevic A.;
 RT "Reconstruction and analysis of human Alu genes.";
 RL J. Mol. Evol. 32:10-12(1991).
 CC -!- MISCELLANEOUS: ISOLATED 'X' INDICATES THE PRESENCE OF A STOP CODON. 'XXX' IS USED TO SEPARATE THE VARIOUS TRANSLATION PHASES.
 CC -!- CAUTION: THIS ALU ENTRY IS PROVIDED IN ORDER TO AVOID THE FURTHER POLLUTION OF PROTEIN SEQUENCE DATABASES WITH ALU-DERIVED AMINO ACID SEQUENCES.

RESULT 10 YA17_SCBPO STANDARD; PRT; 561 AA.
 AC Q09894;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein C24B11.07C in chromosome 1.
 GN SPAC24B11.07C.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota: Fungi: Ascomycota: Schizosaccharomycetes;
 OC Schizosaccharomycetales: Schizosaccharomycetaceae;
 OC Schizosaccharomyces.
 OC NCBI_TAXID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=972;
 RA Odeil C., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;

CC -!- CAUTION: ALU REPETITIVE SEQUENCES ARE interspersed in human and
CC PRIMATE GENOMES WITH AN AVERAGE SPACING OF 4 KB. SOME OF THEM ARE
CC ACTIVELY TRANSCRIBED BY POL I, IT, NORMAL TRANSCRIPTS MAY CONTAIN
CC ALU-DERIVED SEQUENCES IN 5' OR 3' UNTRANSLATED REGIONS. HOWEVER,
CC CDNA LIBRARIES ALSO CONTAIN PARTIAL AND/OR REARRANGED CDNAS
CC LIGATED WITH ALU-DERIVED SEQUENCE IN ANY ORIENTATION. ALTHOUGH ALU
CC ELEMENTS (ESPECIALLY SITUATED ON THE COMPLEMENTARY STRAND) HAVE A
CC GREAT POTENTIAL TO CREATE ADDITIONAL/ALTERNATIVE EXONS,
CC CONSIDERATION SHOULD BE GIVEN TO THE POSSIBILITY THAT THE PRESENCE
CC OF AN ALU IN AN OPEN READING FRAME MAY HAVE RESULTED FROM A
CC CLONING ARTIFACT OR MAY BE DUE TO MISINTERPRETATION OF SEQUENCING
CC DATA. THIS POINT HAS BEEN OVERLOOKED ON SEVERAL OCCASIONS, WITH
CC THE CONSEQUENCE OF ERRONEOUS ALU-DERIVED AMINO ACID SEQUENCES
CC BEING REPORTED.
CC -!- CAUTION: ANY SIGNIFICANT SIMILARITY OF A PUTATIVE PROTEIN SEQUENCE
CC WITH AN ALU-TRANSLATED ENTRY MUST BE TAKEN AS A WARNING THAT A
CC PART OF ALU REPEAT MAY HAVE BEEN ARTIFACTUALLY INCLUDED IN THE
CC CODING NUCLEOTIDE SEQUENCE.

CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U14567; -; NOT_ANNOTATED_CDS.
DR HYPOTHETICAL PROTEIN_96.
FT DOMAIN 1. FRAME-1.
FT DOMAIN 100. FRAME-2.
FT DOMAIN 199. FRAME-3.
FT DOMAIN 298. FRAME-4.
FT DOMAIN 397. FRAME-5.
FT DOMAIN 496. FRAME-6.
SQ SEQUENCE 591 AA; 63790 MW; 6650395335519b95 CRC64;

Query Match 89.7%; Score 26; DB 1; Length 591;
Best Local Similarity 83.3%; Pred. No. 1.4e+02; Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LEPRSS 6 ||||:
Db 22 LEPRSS 27

RESULT 12
PKN6_MYXHA
ID PRN6_MYXHA STANDARD: PRT; 710 AA.
AC P54738;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Serine/threonine-protein kinase pkn6 (EC 2.7.1. -).
GN PKN6.
OS Myxococcus xanthus.
OC Bacteria; Proteobacteria; delta subdivision; Myxobacteria;
OC Myxococcales; Cystobacterineae; Myxoccaceae; Myxococcus.
OX NCBI_TaxID=34;
RN [1]
RP SEQUENCE FROM N.A.
RT STRAIN=DZFL;
RX MEDLINE=96310380; PubMed=8733241;
RA Zhang W., Inouye M., Inouye S.;
RT "Reciprocal regulation of the differentiation of Myxococcus xanthus
by pkn5 and pkn6, eukaryotic-like Ser/Thr protein kinases.",
RT Mol. Microbiol. 20:435-447 (1996).
-!- FUNCTION: PRN6 AND PKN6 MAY HAVE RECIPROCAL ROLES IN GROWTH AND
DEVELOPMENT. PKN6 MAY BE A TRANSMEMBRANE SENSOR OF EXTERNAL
CC SIGNALS FOR DEVELOPMENT.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -----
CC -!- DEVELOPMENTAL STAGE: EXPRESSED CONSTITUTIVELY THROUGHOUT THE LIFE

CC CYCLE, WITH SLIGHT INCREASES AT AN EARLY STAGE OF DEVELOPMENT.
CC -!- PTM: AUTOPHOSPHORYLATED AT SERINE AND THREONINE RESIDUES.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U40656; AAB40050.1; -.
DR HSSP; P00523; 2PTK.
DR InterPro; IPR00719; Euk_Pkinase.
DR InterPro; IPR024290; Ser_thr_Pkinase.
DR PRAM; P00059; Pkinase_1.
DR PROSITE; PS00108; PROTEIN_KINASE_ATP; FALSE_NEG.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; FALSE_NEG.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM_1.
KW Transfase; serine/threonine-protein kinase; ATP-binding;
KW transmembrane; Phosphorylation; Repeat.
FT DOMAIN 1.482 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 483 503 POTENTIAL.
FT DOMAIN 504 710 PERIPLASMIC (POTENTIAL).
FT DOMAIN 6 280 PROTEIN KINASE.
FT NP-BIND 12 ATP (BY SIMILARITY).
FT BINDING 38 ATP (BY SIMILARITY).
FT ACT_SITE 143 143 BY SIMILARITY.
FT DOMAIN 337 369 2 X 12 AA REPEAT OF P-V/A-D-S-T-S-P-T-
FT REPEAT 337 348 P-M-P.
FT REPEAT 358 369 1.
FT REPEAT 358 369 2.
SQ SEQUENCE 710 AA; 74621 MW; 2. EDCF670072DCBAA CRC64;

Query Match 89.7%; Score 26; DB 1; Length 710;
Best Local Similarity 83.3%; Pred. No. 1.7e+02; Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LEPRSS 6 ||||:
Db 379 LEPRSS 384

RESULT 13
CAN3_RAT
ID CAN3_RAT STANDARD: PRT; 821 AA.
AC P16259;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Calpain 3 large subunit (EC 3.4.22.17) (Calpain L3) (Calpain p94',
DE large [catalytic] subunit) (Calcium-activated neutral protease 3)
DE (CANP 3) (muscle-specific calcium-activated neutral protease 3 large
DE subunit).
GN CANP3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Skeletal muscle;
RX MEDLINE=90062125; PubMed=2555341;
RA Sorimachi H., ImaJoh-Ohmi S., Emori Y., Kawasaki H., Ohno S.,
RA Minami Y., Suzuki K.;
RT "Molecular cloning of a novel mammalian calcium-dependent protease
RT distinct from both m- and mu-types. Specific expression of the mRNA
RT in skeletal muscle.", J. Biol. Chem. 264:20106-20111(1989).
RL -!- FUNCTION: Calcium-regulated non-lysosomal thiol-protease.
CC -----
CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Tyr-| -xaa, Met-| -xaa or

RT complementation on a peroxisome-deficient mammalian cell mutant.";
 RL Nat. Genet. 11:395-401(1995).
 RN [2]
 RP SEQUENCE FROM N. A.
 RC STRAIN=SPRAGUE-DAWLEY;
 RA Tsukamoto T; Hashiguchi N.;
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 CC -I- FUNCTION: INVOLVED IN PEROXISOME BIOSYNTHESIS. REQUIRED FOR
 CC STABILITY OF THE PTS1 RECEPTOR.
 CC -I- SUBCELLULAR LOCATION: PERIPHERAL MEMBRANE PROTEIN, PEROXISOME.
 CC -I- SIMILARITY: BELONGS TO THE AAA FAMILY OF ATPSES.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC use by non-profit institution as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; D63673; BAA09824.1; -.
 DR EMBL; D89660; BAA24931.1; -.
 DR EMBL; D89657; BAA24931.1; JOINED.
 DR EMBL; D89658; BAA24931.1; JOINED.
 DR EMBL; D89659; BAA24931.1; JOINED.
 DR InterPro; IPR003593; AAA.
 DR InterPro; IPR003960; AAA_sub.
 DR InterPro; IPR003959; AAA_subAm.
 DR Pfam; PF00004; AAA; 2.
 DR SMART; SM00382; AAA; 1.
 DR PROSITE; PS00574; AAA; 1.
 KW Peroxisome; ATP-binding; Repeat.
 FT NP_BIND 470 477 ATP (POTENTIAL).
 FT NP_BIND 742 749 ATP (POTENTIAL).
 FT MUTAGEN 476 476 K->A: NO LOSS OF FUNCTION.
 FT MUTAGEN 748 748 K->A: LOSS OF FUNCTION.
 FT CONFLICT 299 299 D -> G (IN REF. 2)
 FT CONFLICT 333 333 V -> A (IN REF. 2).
 FT CONFLICT 343 343 Q -> R (IN REF. 2).
 FT CONFLICT 546 546 R -> C (IN REF. 2).
 SQ SEQUENCE 978 AA; 104426 MW; F723198B7E95EA97 CRC64;

Query Match 89 7%; Score 26; DB 1; Length 978;
 Best Local Similarity 83 3%; Pred. No. 2.4e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEPRAS 6
 DB 935 LEPRSS 940

Search completed: June 6, 2002, 13:08:09
 Job time: 211 sec

THIS PAGE BLANK (USPTO)

GenCore version 4.5
copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 6, 2002, 13:04:13 ; Search time 25.04 Seconds

(without alignments) 41.452 Million cell updates/sec

Title: US-09-627-383-1

Perfect score: 29

Sequence: 1 LEPRAS 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 0

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPREMBL_19:*

- 1: sp_archea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rabbit:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description	RESULT	1	ALIGNMENTS
1	29	100.0	162	16	Q9RTL2	Q9rtl2 deinococcus	Q9RTL2	PRELIMINARY;	PRT; 162 AA.
2	29	100.0	242	16	Q9PCP1	Q9pcp1 xylella fas	Q9RTL2;		
3	29	100.0	526	4	Q9NUY2	Q9nuy2 homo sapien	Q9RTL2;		
4	29	100.0	594	10	Q9LGZ7	Q9lgz7 oryza sativ	Q9RTL2;		
5	29	100.0	635	5	Q24564	Q24564 drosophila	Q9RTL2;		
6	29	100.0	1060	5	Q46055	Q46055 drosophila	Q9RTL2;		
7	29	100.0	1077	5	Q9V8H8	Q9v8h8 drosophila	Q9RTL2;		
8	29	1397	4	Q9NTG2	Q9ntg2 homo sapien	Q9RTL2;			
9	29	100.0	2359	11	Q9EQ60	Q9eq60 ratto norv	Q9RTL2;		
10	29	100.0	2548	4	Q9UNJ2	Q9unj2 homo sapien	Q9RTL2;		
11	29	100.0	2626	11	Q9Z1N3	Q9z1n3 rattus norv	Q9RTL2;		
12	27	93.1	311	2	Q68976	Q68976 brucella me	Q9RTL2;		
13	27	93.1	356	16	Q986C9	Q986c9 rhizobium l	Q9RTL2;		
14	27	93.1	357	7	Q95560	Q95560 peromyscus	Q9RTL2;		
15	27	.93.1	357	7	Q95410	Q95410 hylobates l	Q9RTL2;		
16	27	.93.1	357	7	Q95411	Q95411 hylobates l	Q9RTL2;		

RESULT	2	OX NCBI_TaxID=9606;
Q9PCP1	PRELIMINARY;	RN [1]
ID Q9PCP1	PRT; 242 AA.	RP SEQUENCE FROM N.A.
AC Q9PCP1;		RC TISSUE=PLACENTA;
DT 01-OCT-2000 (TREMBLREL. 15, Created)		RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagai K., Sugano S., Aotsuka S., Yoshikawa Y., Matsumura H., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahashi K., Masuho Y., Sasaki N.;
DT 01-OCT-2000 (TREMBLREL. 15, Last sequence update)		RA "NECD human cDNA sequencing Project.";
DT 01-DEC-2001 (TREMBLREL. 19, Last annotation update)		RT Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DE HYPOTHETICAL PROTEIN XFL1737.		RL EMBL: AK01923; BAA91979; 1.;
GN XFL1737.		DR HSSP: Q07960; 1RGP.
OS Xylella fastidiosa.		DR InterPro: IPR001018; RhoGAP; 1.
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group; OX Xylella.		DR SMART: SM00324; RhoGAP; 1.
OC Xylella fastidiosa.		DR SEQUENCE 526 AA; 59212 MW; 868624871E4C860C CRC64;
RN		SQ
RP SEQUENCE FROM N.A.		
RC STRAIN=945C;		
RX MEDLINE=20365717; PubMed=10301347;		
RA SIMPSON A.J.G., Reinach F.C., Arruda P., Abreu F.A., Aceñolí M., Alvaengua R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S., Barrios M.H., Bonacorsi E.D., Bordin S., Bove J.M., Briones M.R.S., Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H., Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M., Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H., Facincani A.P., Ferreira A.C.A., Ferreiro J.A., Fraga J.S., França S.C., Franco M.C., Frohne M., Furian L.R., Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A., Ho P.L., Hoheisel J.D., Jungueira J.P., Kitzojima J.P., Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C., Lemos E.G.M., Lemos M.F., Lopes S.A., Lopes C.R., Machado J.A., Machado M.A., Madiira A.M.B.N., Madeira H.M.F., Marino C.L., Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y., Menck C.F.M., Miracins E.C., Miyaki C.Y., Monteiro-Vitalelo C.B., Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S., Nhani A.Jr., Nobreaga F.G., Nunes L.R., Oliveira M.A., Oliveira M.C., Oliveira R.C., Palmeri D.A., Paris A., Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B., Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M., Rosa V.E. Jr., de Sa R.G., Santelli R.V., Swasaki H.E., da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr., da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A., de Souza A.P., Terenzio M.F., Truffi D., Tsai S.M., Tshukao M.H., Vaiheda H., Van Sluys M.A., Verjovskiy-Almeida S., Vettore A.L., Zago M.A., Zatz M., Meidanis J., Setubal J.C.;		
RT "The genome sequence of the plant pathogen <i>Xylella fastidiosa</i> .";		
RL Nature 406:151-155 (2000).		
DR EMBL: AP003997; RAB4546.1; -.		
KW Hypothetical protein; Complete proteome.		
SQ SEQUENCE 242 AA; 25385 MW; 857F70152F2B0C1B CRC64;		
Query Match 100.0%; Score 29; DB 16; Length 242;		
Best Local Similarity 100.0%; Pred. No. 43;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY 1 LEPRAS 6		
Db 75 LEPRAS 80		
RESULT 3		
Q9NUY2 PRELIMINARY; PRT; 526 AA.		
ID Q9NUY2		
AC Q9NUY2;		
DT 01-OCT-2000 (TREMBLREL. 15, Created)		
DT 01-OCT-2000 (TREMBLREL. 15, Last sequence update)		
DT 01-DEC-2001 (TREMBLREL. 19, Last annotation update)		
DE CINA FUJI1101 F1S, CLONE PLACE1004777, WEAKLY SIMILAR TO N-CHIMARIN		
OS Homo sapiens (Human).		
OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydioidea; Dirosophilidae; Dirosophila;		
RN [1]		
RP SEQUENCE FROM N.A.		
RC TISSUE=PLACENTA;		
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagai K., Sugano S., Aotsuka S., Yoshikawa Y., Matsumura H., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahashi K., Masuho Y., Sasaki N.;		
RA "NECD human cDNA sequencing Project.";		
RT Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.		
RL EMBL: AK01923; BAA91979; 1.;		
DR HSSP: Q07960; 1RGP.		
DR InterPro: IPR001018; RhoGAP; 1.		
DR SMART: SM00324; RhoGAP; 1.		
DR SEQUENCE 526 AA; 59212 MW; 868624871E4C860C CRC64;		
Query Match 100.0%; Score 29; DB 10; Length 594;		
Best Local Similarity 100.0%; Pred. No. 1.1e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY 1 LEPRAS 6		
Db 218 LEPRAS 223		
RESULT 5		
Q24564 PRELIMINARY; PRT; 635 AA.		
ID Q24564		
AC Q24564; Q24564;		
DT 01-NOV-1996 (TREMBLREL. 01, Created)		
DT 01-NOV-1996 (TREMBLREL. 01, Last sequence update)		
DT 01-JUN-2001 (TREMBLREL. 17, Last annotation update)		
DE MER PROTEIN (CYTOSKELETON PROTEIN).		
DE MER OR EMBR2 OR DMERLIN OR CG14228.		
OS Drosophila melanogaster (Fruit Fly).		
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;		
OC Ephydioidea; Dirosophilidae; Dirosophila;		

NCBI_TAXID=7227;	QY	1	LEPRAS	6
[1]				
SEQUENCE FROM N.A.				
RN	RP	27	LEPRAS	32
RESTRN	RESULT	6		
RX	ID	06055	PRELIMINARY;	PRN;
STRAIN=BERKELEY;	AC	06055;		1060 AA.
MEDLINE=20196006; PubMed=10731132;	DT	01-JUN-1998 (TREMBLrel. 06, Created)		
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,	DT	01-NOV-1999 (TREMBLrel. 12, Last sequence update)		
Amatiades P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,	DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)		
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,	DE	EG:165H7.3 PROTEIN.		
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,	GN	L(1)1BB OR EG:165H7.3 OR CG3923.		
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champé M., Pfeiffer B.D.,	OS	Drosophila melanogaster (Fruit fly).		
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,	OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;		
Abrial J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,	OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;		
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,	OC	Ephydriidea; Drosophilidae; Drosophila.		
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,	OX	NCBI_TAXID=7227;		
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,	RN	[1]		
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,	RP	SEQUENCE FROM N.A.		
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,	RA	de Pablos B., Madueno E., Modolell J.;		
de Pablos B., Madueno E., Modolell J.;	RA	"Sequencing the distal X chromosome of Drosophila melanogaster. "		
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,	RA	Submitted (PBC-1997) to the EMBL/GenBank/DBJ databases.		
Kimmel B.E., Koira C.D., Kraft C., Kravitz C., Kulp D., Lai Z.,	RA	[2]		
Lasko P., Lei Y., Levitsky D., Li Z., Liang Y., Lin X.,	RA	SEQUENCE FROM N.A.		
Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,	RA	de Pablos B., Madueno E., Modolell J.;		
Merkulov G., Milshina N.V., Moarry C., Morris J., Mosnati A.,	RA	"Sequencing the distal X chromosome of Drosophila melanogaster. "		
Mount S.M., Moy M., Murphy B., Muzyk D.M., Nelson D.L.,	RA	Submitted (PBC-1997) to the EMBL/GenBank/DBJ databases.		
Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclob J.M.,	RA	[1]		
Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,	RA	SEQUENCE FROM N.A.		
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,	RA	de Pablos B., Madueno E., Modolell J.;		
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,	RA	"Sequencing the distal X chromosome of Drosophila melanogaster. "		
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,	RA	Submitted (PBC-1997) to the EMBL/GenBank/DBJ databases.		
Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,	RA	[2]		
Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,	RA	SEQUENCE FROM N.A.		
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,	RA	de Pablos B., Madueno E., Modolell J.;		
Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,	RA	"Sequencing the distal X chromosome of Drosophila melanogaster. "		
Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,	RA	Submitted (PBC-1997) to the EMBL/GenBank/DBJ databases.		
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,	RA	EMBL; AI009188; CA15674.2; -.		
The genome sequence of Drosophila melanogaster. ;	RA	DR		
RT	DR	InterPro; IPR01494; IBNLNT.		
RL	DR	SEQUENCE; 1060 AA; 119276 MW; 650B03CD25DB9156 CRC64;		
RN	DR	CG12263. PROTEIN.		
SEQUENCE FROM N.A.	DR	CG12263.		
RN	DR	Drosophila melanogaster (Fruit fly).		
SEQUENCE OF 218-307 FROM N.A.	DR	OC		
RN	DR	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;		
RL	DR	Prerygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;		
EMBL; AED03512; AAF49005.1; -.	DR	OC		
EMBL; U49124; AAB08449.1; -.	DR	Ephydriidea; Drosophilidae; Drosophila.		
FlyBase; FBgn0013951; Mer.	DR	OC		
INTERPRO; IPR000299; Band.4.1.	DR	NCBI_TAXID=7227;		
INTERPRO; IPR000798; Ezrin_radixin_moesin.	DR	RN		
PFAM; PF001373; Band.41; 1.	DR	SEQUENCE FROM N.A.		
PFAM; PF00769; ERM; 1.	DR	RN		
PRINTS; PR00935; BAND41.	DR	SEQUENCE FROM N.A.		
SMART; SM00295; B41; 1.	DR	RN		
PROSITE; PS50057; BAND41_3; 1.	DR	SEQUENCE FROM N.A.		
SEQUENCE; 635 AA; 74492 MW; 940DBB8A00160A3F CRO64;	DR	RN		
Query Match 100.0%; Score 29; DB 5; Length 635;	RN	SEQUENCE FROM N.A.		
Best Local Similarity 100.0%; Pred. No. 1.1e02;	RN	RX		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	RN	NCBI_TAXID=7227;		

Query Match 100.0%; Score 29; DB 4; Length 2548;
 Best Local Similarity 100.0%; Pred. No. 4.5e+02; Length 2626;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEPRAS 6
 Db 2357 LEPRAS 2362

RESULT 11

PRELIMINARY; PRT; 2626 AA.

ID Q9Z1N3
 AC Q9Z1N3;
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE MYOSIN-RHOGAP PROTEIN MYR 7.

GN MY09A

OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]

SEQUENCE FROM N.A.

RA Chieregatti E., Gaertner A., Stoeffler H.E., Baehler M.;
 RT "Myr 7 is a novel myosin-Rho-GAP molecule expressed in rat brain.";
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ001713; CAA04946.1; -.
 DR HSSP; IMND;
 DR Interpro; IPR002106; AA_tRNA_ligase_II.
 DR Interpro; IPR002219; DAG_Pe-bind.
 DR Interpro; IPR00048; IQ.
 DR Interpro; IPR001609; myosin_head.
 DR InterPro; IPR000159; RA.
 DR InterPro; IPR000198; Rhogap.
 DR pfam; PF00130; DAG_Pe-bind; 1.
 DR pfam; PF00612; IQ; 5.
 DR pfam; PF00063; myosin_head; 2.
 DR pfam; PF00788; RA; 1.
 DR pfam; PF00620; Rhogap; 1.
 DR PRINTS; PR00193; MYOSINHEAVY.
 DR PRODOM; PD000355; myosin_head; 2.
 DR SMART; SM0015; C1; 5.
 DR SMART; SM00242; MYSIC; 1.
 DR SMART; SM00314; RA; 1.
 DR PROSITE; PS00179; AA_TRNA_LIGASE_II_1; UNKNOWN_1.
 DR PROSITE; PS00479; DAG_Pe_BIND_DOM_1; UNKNOWN_1.
 DR PROSITE; PS50081; DAG_Pe_BIND_DOM_2; 2.
 SQ SEQUENCE 2548 AA; 292703 MW; B93B76C2A0E9A356 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 311;
 Best Local Similarity 83.3%; Pred. No. 1.7e+02; Length 309;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEPRAS 6
 Db 173 MPRAS 178

RESULT 13

PRELIMINARY; PRT; 356 AA.

ID Q986C9
 AC Q986C9;
 DT 01-OCT-2001 (TREMBLrel. 18, Created)
 DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
 DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
 DE MLL7417 PROTEIN.

GN MLL7417.

OS Rhizobium loti (Mesorhizobium loti).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Phyllobacteriaceae; Mesorhizobium.
 OX NCBI_TaxID=381;

SEQUENCE FROM N.A.

RA SISTRAINMAFF03099;
 RX MEDLINE=21082930; PubMed=11214968;
 RA Kaneko T., Nakamura Y., Sato S., Asanizu E., Kato T., Sasamoto S.,
 RA Watanabe A., Idezawa K., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kiyosawa C., Kohara M., Matsunoto M., Matsuno A.,
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shimo S., Sugimoto M.,
 RA Takeuchi C., Yamada M., Tabata S.;
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
 Mesorhizobium loti.";

Query Match 93.1%; Score 27; DB 7; Length 357;
 Best Local Similarity 83.3%; Pred. No. 1.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LEPRAS 6
 :|||||
 Db 66 MEPRAS 71

RESULT 14

Q95560 PRELIMINARY; PRM; 357 AA.

095560: (TREMBLrel. 02, Created)
 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

PERMYSCUS MANICULATUS (Deer mouse).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates;
 Peromyscus; Rodentia; Sciurognath; Muridae; Sigmodontinae;
 NCBI_TaxID=10042;
 [1]
 RN SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE=96289997; PubMed=8662082;
 RA Crew M.D., Batten L.M., Douglass C.A., York J.L.;
 RT "Expressed Peromyscus maniculatus (Peromyscus) MHC class I genes:
 evolutionary implications and the identification of a gene encoding a
 Qa-like antigen.", Immunogenetics 44:177-185 (1996).
 RL -
 CC -
 -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE
 IMMUNE SYSTEM (BY SIMILARITY).
 CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 MICROGLOBULIN) (BY SIMILARITY).
 DR EMBL: U50089; AAB0072.1; -.
 DR HSSP: O19673; IHSB.
 DR InterPro: IPR003597; Ig_c1.
 DR InterPro: IPR00306; Ig_MHC.
 DR InterPro: IPR001039; MHC_I.
 DR Pfam: PF00047; Ig; 1.
 DR Pfam: PF00129; MHC_I; 1.
 DR Pfam: PF00050; MHC_I; 1.
 DR SMART: SM00407; IgC1; 1.
 DR PROSITE: PS00290; Ig_MHC; 1.
 DR KW Glycoprotein; Transmembrane.
 FT NON_TER 1
 SQ SEQUENCE 357 AA; 40223 MW; 682DDDFBEB8DB9F361 CRC64;

Query Match 93.1%; Score 27; DB 7; Length 357;
 Best Local Similarity 83.3%; Pred. No. 1.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LEPRAS 6
 :|||||
 Db 61 MEPRAS 66

Search completed: June 6, 2002, 13:07:53
 Job time: 220 sec

RESULT 15

Q95410 PRELIMINARY; PRT; 357 AA.

095410: (TREMBLrel. 02, Created)
 01-FEB-1997 (TREMBLrel. 02, Last sequence update)

Query Match 93.1%; Score 27; DB 7; Length 357;
 Best Local Similarity 83.3%; Pred. No. 1.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LEPRAS 6
 :|||||
 Db 66 MEPRAS 71

THIS PAGE BLANK (USPTO)